



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 174325**

**TO: Patricia Duffy**  
**Location: REM-3B05/3C18**  
**Art Unit: 1645**  
**Thursday, December 22, 2005**

**Case Serial Number: 10/077137**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**REM-1A65**  
**Phone: 571-272-2527**

**Paul.schulwitz@uspto.gov**

### **Search Notes**

Examiner Duffy,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
REM-1A65  
571-272-2527

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From: Duffy, Patricia  
Sent: Thursday, December 15, 2005 9:06 AM  
To: STIC-Biotech/ChemLib  
Subject: SEQUENCE SEARCH 10/077,137

IN RE: 10/077,137

PLEASE SEARCH RESIDUES 1-51 OF SEQ ID NO:1.  
PLEASE SEARCH RESIDUES 8-41 OF SEQ ID NO:1

PLEASE SEARCH BOTH COMMERCIAL AND INTERFERENCE DATABASES.  
PLEASE PRINT OUT TOP 75 HITS IN EACH CATEGORY.

THANKS MUCHO.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

RECEIVED  
DEC 15 2005  
STIC-BIOTECH/CHMLIB  
(STIC)

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 15:43:09 ; Search time 159.6 Seconds  
(without alignments)  
140.403 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51

Perfect score: 283

Sequence: 1 MLAGQCSQNEYPFSLHA.....TPPLTCQRCYNASVTNSVKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A Geneseq 21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	52	9	AEC02032 Amino aci
2	283	100.0	184	3	AAB08843 Amino aci
3	283	100.0	184	3	AAY94001 A human B
4	283	100.0	184	4	AAB09241 Human BCM
5	283	100.0	184	4	AAY71979 Human B C
6	283	100.0	184	4	AAB60698 Human BAF
7	283	100.0	184	4	AAB00506 Human B C
8	283	100.0	184	5	ABB81487 Human BCM
9	283	100.0	184	5	ABP54694 Metastati
10	283	100.0	184	5	AAB28961 Human B-C
11	283	100.0	184	6	AAB35216 Human B-C
12	283	100.0	184	6	ADA49361 Human BCM
13	283	100.0	184	6	ABP60552 Human tum
14	283	100.0	184	6	ABP97717 Amino aci
15	283	100.0	184	7	ADD67527 Human Lyl
16	283	100.0	184	7	ADG43715 Human B-C
17	283	100.0	184	8	ADK00756 Native hu
18	283	100.0	184	8	ADQ94442 Neutrokin
19	283	100.0	184	8	ADP56014 Human PRO
20	283	100.0	184	9	ADW03432 Human BCM
21	283	100.0	184	9	ADZ67760 Human tum
22	283	100.0	184	9	AEA23348 Tumor ant
23	283	100.0	184	9	AEC02031 Amino aci
24	283	100.0	302	4	AAB60699 Mouse Igg

25	283	100.0	302	4	AAE00507 Human BCM
26	283	100.0	302	7	ADG43717 Human B-C
27	277	97.9	184	6	ABR40082 Human Gen
28	274	96.8	288	5	ABG95060 Human tra
29	269	95.1	51	5	AAE15485 Human B-C
30	269	95.1	181	5	AAE15484 Human B-C
31	269	95.1	283	5	AAE15488 Human BCM
32	257	90.8	296	9	AEC02042 Amino aci
33	249	88.0	58	5	AAE15501 Human B C
34	230	81.3	40	9	ADZ67761 Human tum
35	215	78.0	38	9	AEC02033 Amino aci
36	206	72.8	157	4	ABE07000 Human BAF
37	201	71.0	34	5	AAE15486 Human B-C
38	201	71.0	34	6	ADA49366 Human BCM
39	197	69.6	34	9	AEC02026 Formula I
40	196	69.3	34	9	AEC02027 Formula I
41	194	68.6	34	9	AEC02028 Formula I
42	194	68.6	34	9	AEC02017 Formula I
43	192	67.8	34	9	AEC02025 Formula I
44	192	67.8	34	9	AEC02024 Formula I
45	191	67.5	34	9	AEC02020 Formula I
46	189	66.8	34	9	AEC02018 Formula I
47	189	66.8	34	9	AEC02029 Formula I
48	182	64.3	185	3	AAB08844 Amino aci
49	181	64.0	185	3	AAE15490 Murine B
50	181	64.0	185	5	AAE15490 Mouse B C
51	181	64.0	185	5	AAE15490 Mouse B C
52	181	64.0	185	9	ADZ67762 Mouse tum
53	181	64.0	281	5	AAE15489 Mouse BCM
54	158	55.8	42	6	ABJ38417 TALL-1 re
55	151	53.4	26	7	AD153060 Human BCM
56	104	36.7	117	5	AAE15491 Human-mur
57	90.5	32.0	24	5	AAE15492 Human-mur
58	71.5	25.3	249	3	AAE15492 A murine
59	71.5	25.3	249	7	ABM85744 Mouse pro
60	71.5	25.3	249	9	ADZ67773 Mouse tum
61	71.5	25.3	249	9	AEAS5078 Tumor nec
62	70.5	24.9	1548	7	ADC71568 Murine su
63	70.5	24.9	1877	7	ABB80243 Murine su
64	68.5	24.2	332	6	AAE35228 Human TAC
65	68.5	24.2	1569	8	ADR18921 Human muc
66	68.5	24.2	2240	8	ADR18914 Mature Hu
67	68.5	24.2	2258	8	ADR18913 Human muc
68	68.5	24.2	2264	8	ADR18915 H1e-tagge
69	67.5	23.9	37	5	AAU10951 Human AGP
70	67.5	23.9	48	9	ADZ67772 Human tum
71	67.5	23.9	59	5	AAE15500 Human TAC
72	67.5	23.9	166	2	AAW75785 Human TAC
73	67.5	23.9	166	5	AAE15494 Human TAC
74	67.5	23.9	171	8	ADN03188 Human TAC
75	67.5	23.9	265	4	AAE09244 Human TAC
76	67.5	23.9	266	6	ABP97723 Amino aci
77	67.5	23.9	266	9	ADW03442 Human TAC
78	67.5	23.9	291	5	AAU10949 Human AGP
79	67.5	23.9	292	9	ADZ67771 Human tum
80	67.5	23.9	293	2	AAW75783 Human tum
81	67.5	23.9	293	3	AAW75783 Human lymph
82	67.5	23.9	293	3	AAE15494 Human TAC
83	67.5	23.9	293	4	AAE09240 Human TAC
84	67.5	23.9	293	4	AAO14130 Human tra
85	67.5	23.9	293	5	AAO14130 Human tra
86	67.5	23.9	293	5	ABB81488 Human TAC
87	67.5	23.9	293	5	AAU99512 Human TAC
88	67.5	23.9	293	5	AAU99512 Human TAC
89	67.5	23.9	293	5	AAU99512 Human TAC
90	67.5	23.9	293	5	AAU99512 Human TAC
91	67.5	23.9	293	5	AAU99512 Human TAC
92	67.5	23.9	293	5	AAU99512 Human TAC
93	67.5	23.9	293	5	AAU99512 Human TAC
94	67.5	23.9	293	6	ABE35211 Human tra
95	67.5	23.9	293	6	ABE35211 Human tra
96	67.5	23.9	293	6	ABP60551 Human tum
97	67.5	23.9	293	6	ABP97716 Amino aci
98	67.5	23.9	293	6	AAO29592 Human DIT
99	67.5	23.9	293	7	ADF72628 Human tum

98	67.5	23.9	293	7	ADF77379	Adf77379 Human tum	171	63	22.3	175	9	AEA01659	Aea01659 B-cell ac
99	67.5	23.9	293	7	ABM85745	Abm85745 Human pro	172	63	22.3	314	9	ADW03396	Adv03396 Mouse BR3
100	67.5	23.9	293	8	ADX00754	Adx00754 Native hu	173	63	22.3	316	9	AEA01660	Abu01660 Murine BA
101	67.5	23.9	293	8	ADJ92514	Adj92514 Human TAC	174	63	22.3	1887	6	ABU12113	Abu12113 Human pro
102	67.5	23.9	293	8	ADN03174	Adn03174 Human TAC	175	63	22.3	1887	7	ABB80242	Abb80242 Human sub
103	67.5	23.9	293	8	ADQ76815	Adq76815 Human TAC	176	63	22.3	1887	7	ADM29324	Adm29324 Human nov
104	67.5	23.9	293	8	ADQ94440	Adq94440 Neutrokin	177	62.5	22.1	138	5	ABP69063	Abp69063 Human pol
105	67.5	23.9	293	8	ADW03430	Adw03430 Human TAC	178	62.5	22.1	558	8	AQO82379	Aqo82379 Novel hum
106	67.5	23.9	294	8	ADK00765	Adk00765 Htaci epl	179	62.5	22.1	775	8	AQO82382	Aqo82382 Fibulin-1
107	67.5	23.9	294	8	ADW03443	Adw03443 Human TAC	180	62.5	22.1	818	8	AQO82380	Aqo82380 Fibulin-1
108	67.5	23.9	312	5	AAO14135	Aao14135 Protein o	181	62.5	22.1	818	8	AQO82377	Aqo82377 Novel hum
109	67.5	23.9	334	5	AAO14133	Aao14133 Protein o	182	62.5	22.1	818	8	AQO82383	Aqo82383 Fibulin-1
110	67.5	23.9	344	6	AAE35224	Aae35224 Human TAC	183	62.5	22.1	985	7	ADMO4189	Adm04189 Human pro
111	67.5	23.9	348	6	AAE35225	Aae35225 Human TAC	184	62.5	22.1	992	7	AAE38809	Aae38809 Human POL
112	67.5	23.9	357	6	AAE35226	Aae35226 Human TAC	185	62.5	22.1	999	8	ADN23019	Adn23019 Bacterial
113	67.5	23.9	366	5	AAO14132	Aao14132 Protein o	186	62.5	22.1	999	8	ADN23018	Adn23018 Bacterial
114	67.5	23.9	392	6	AAE35223	Aae35223 Human TAC	187	61.5	21.7	99	5	AAO21327	Aao21327 Arabidops
115	67.5	23.9	397	5	AAE15498	Aae15498 Human TAC	188	61.5	21.7	99	8	ADG74883	Adg74883 Plant dev
116	67.5	23.9	404	5	AAO14136	Aao14136 Protein o	189	61.5	21.7	99	8	ADJ63800	Adj63800 Plant lip
117	67.5	23.9	1994	8	ADR18912	Adr18912 Human muc	190	61.5	21.7	353	4	ABB71555	Abb71555 Drosophil
118	66.5	23.5	33	5	AAE15495	Aae15495 Human TAC	191	61.5	21.7	798	4	ABB6495	Abb6495 Drosophil
119	66.5	23.5	33	6	ADMA9368	Adma9368 Human TAC	192	61	21.6	246	6	ABP97720	Abp97720 Amino aci
120	65	23.0	1895	8	ADM90835	Adm90835 Human pha	193	61	21.6	246	8	ADK00762	Adk00762 Native hu
121	65	23.0	2417	8	ADH71332	Adh71332 Human pro	194	61	21.6	246	9	ADW03438	Adw03438 Human TAC
122	65	23.0	2420	5	ABJ10587	Abj10587 Human nov	195	61	21.6	247	3	AAV93998	Aav93998 Human BR4
123	65	23.0	2420	8	ADQ09838	Ado09838 Human NOV	196	61	21.6	247	7	ABR61797	AbR61797 Human RYZ
124	65	23.0	2551	8	ADH71360	Adh71360 Human pro	197	60.5	21.4	40	9	AEC02013	Aec02013 Formula I
125	65	23.0	2675	5	ABJ10586	Abj10586 Human nov	198	60.5	21.4	1417	7	ADG39820	Adg39820 Protein s
126	65	23.0	2675	8	ADQ09971	Ado09971 Human NOV	199	60.5	21.4	3034	7	ADG42709	Adg42709 Mouse Cel
127	65	23.0	2675	8	ADQ09836	Ado09836 Human NOV	200	60.5	21.4	3034	7	ADJ55778	Adj55778 Peptide h
128	64.5	22.8	418	5	ABR08238	Abb08238 Human 567	201	60.5	21.4	3034	8	ADM76616	Adm76616 Human NOV
129	64.5	22.8	418	9	ADV54276	Adv54276 Human 567	202	60.5	21.4	3034	8	ADM49429	Adm49429 Mouse sev
130	64.5	22.8	581	7	ADB64650	Adb64650 Human pro	203	60.5	21.4	3034	8	ADN49434	Adn49434 Mouse sev
131	64.5	22.8	735	5	AAQ68258	Aaq68258 Human POL	204	60.5	21.4	3034	8	ADO29244	Ado29244 Mouse GPC
132	64.5	22.8	735	6	ABU12091	Abu12091 Novel hum	205	60	21.2	426	6	ABP55405	Abp55405 Human MDD
133	64.5	22.8	845	5	AAQ68259	Aaq68259 Human POL	206	60	21.2	672	8	ADQ82385	Adq82385 Fibulin-1
134	64.5	22.8	845	6	ABU12092	Abu12092 Novel hum	207	60	21.2	934	8	ADH72262	Adh72262 Human pro
135	64.5	22.8	845	7	AAE38807	Aae38807 Human POL	208	60	21.2	955	6	ADA55084	Ada55084 Human pro
136	64.5	22.8	880	7	ADB64680	Adb64680 Human pro	209	60	21.2	955	6	ADQ82381	Adq82381 Fibulin-1
137	64.5	22.8	897	4	AAQ65887	Aaq65887 Amino aci	210	60	21.2	955	8	AQO82384	Aqo82384 Fibulin-1
138	64.5	22.8	897	4	ABG06309	Abg06309 Novel hum	211	59	20.8	34	5	AAE15496	Aae15496 Human TAC
139	64.5	22.8	897	5	ABG91402	Abg91402 Primate L	212	59	20.8	34	6	ADA49369	Ada49369 Human TAC
140	64.5	22.8	897	7	ADQ07852	Ado07852 Novel pro	213	59	20.8	38	5	AAU10952	Aau10952 Human AGP
141	64.5	22.8	897	7	ADQ08940	Ado08940 Novel pro	214	59	20.8	73	5	AAE22250	Aae22250 Human BAF
142	64.5	22.8	914	8	AD127628	Adi27628 Human SCU	215	59	20.8	73	5	AAE22251	Aae22251 Human BAF
143	64.5	22.8	939	6	AAE29932	Aae29932 Human LP2	216	59	20.8	87	4	AAU41056	Aau41056 Propionib
144	64.5	22.8	973	5	AAQ68260	Aaq68260 Human LP2	217	59	20.8	87	6	ABM37575	Abm37575 Propionib
145	64.5	22.8	974	6	ABU12093	Abu12093 Novel hum	218	59	20.8	266	7	ABO69971	AbO69971 Plasmodi
146	64.5	22.8	974	7	AAE38808	Aae38808 Human POL	219	59	20.8	266	8	ABO69364	AbO69364 Pseudomon
147	64.5	22.8	989	6	AAE30306	Aae30306 Human LP2	220	59	20.8	2459	8	ADO69969	Ado69969 Plasmodi
148	64.5	22.8	991	6	AAO16645	Aao16645 Human ext	221	58.5	20.7	682	7	ADB70224	AdB70224 C. neofo
149	64.5	22.8	993	4	AAQ65888	Aaq65888 Amino aci	222	58.5	20.7	796	4	ABB63128	Abb63128 Drosophil
150	64.5	22.8	993	6	AAE29931	Aae29931 Human LP2	223	58	20.5	124	2	AAW56732	Aaw56732 Nuclellus
151	64.5	22.8	993	8	AD127630	Adi27630 Human SCU	224	58	20.5	271	7	ADJ92151	Adj92151 Human hai
152	64.5	22.8	993	8	AD127637	Adi27637 SCUBE3-2	225	58	20.5	940	8	ADS24125	Ads24125 Bacterial
153	64.5	22.8	1006	5	AAU79172	Aau79172 Human MEG	226	58	20.5	1792	3	ABA48443	AbA48443 Human lam
154	64.5	22.8	1009	5	AAQ68261	Aaq68261 Human POL	227	58	20.5	1800	3	ABA48445	AbA48445 Human lam
155	64.5	22.8	1009	6	AAE29930	Aae29930 Human LP2	228	58	20.5	1816	3	ABA48442	AbA48442 Human lam
156	64.5	22.8	1009	6	ABU12094	Abu12094 Novel hum	229	58	20.5	1816	7	ADC01877	Adc01877 Human lam
157	64	22.6	175	9	ADW03418	Adw03418 Rat BR3 p	230	58	20.5	1816	7	ADCO1879	Adc01879 Human lam
158	64	22.6	175	9	ADM21317	Adm21317 Rat Blys	231	58	20.5	1816	8	ADP08401	Adp08401 Human lam
159	63.5	22.4	428	8	ADQ97204	Adq97204 Mouse can	232	58	20.5	1816	8	ADB87600	AdB87600 Human lam
160	63	22.3	65	5	AAE22247	Aae22247 Mouse BAF	233	58	20.5	1823	5	ABP63020	Abp63020 Human pol
161	63	22.3	67	8	ADT94167	Adt94167 Murine BA	234	58	20.5	1824	3	ABA48444	AbA48444 Human lam
162	63	22.3	128	9	ADZ12994	Adz12994 Murine ca	235	57.5	20.3	76	8	ABO58265	AbO58265 Human gen
163	63	22.3	175	5	ABB78398	Abb78398 Amino aci	236	57.5	20.3	142	7	ADF77377	Adf77377 Human tum
164	63	22.3	175	5	AAE22244	Aae22244 Murine BA	237	57.5	20.3	142	8	ADJ92512	Adj92512 Human TR2
165	63	22.3	175	5	ABB81489	Abb81489 Mouse Ztn	238	57.5	20.3	154	5	AAE29295	Aae29295 Human gen
166	63	22.3	175	6	ABP97722	Abp97722 Amino aci	239	57.5	20.3	499	9	ADW17813	Adw17813 Pinus rad
167	63	22.3	175	9	ADW03417	Adw03417 Murine BR	240	57.5	20.3	499	9	ADW18484	Adw18484 Pinus rad
168	63	22.3	175	9	ADW03444	Adw03444 Murine BR	241	57.5	20.3	508	9	ADW17814	Adw17814 Pinus rad
169	63	22.3	175	9	ADW21300	Adw21300 Mouse Bly	242	57.5	20.3	798	6	ABU58243	Abu58243 Soybean s
170	63	22.3	175	9	ADZ67759	Adz67759 Mouse tum	243	57.5	20.3	1679	4	ABB60498	Abb60498 Drosophil

244	57.5	20.3	1679	4	ABB60502	Abb60502 Drosophil
245	57.5	20.3	1680	8	ADS96568	Ads96568 Drosophil
246	57.5	20.3	1997	5	AU84802	Au84802 KCV Hepc
247	57.5	20.3	2957	4	ABG22214	Abg22214 Novel hum
248	57.5	20.3	5985	5	AAU84799	Aau84799 HCV HepC1
249	57.5	20.1	281	7	AD807963	Ad807963 Novel pro
250	57.5	20.1	281	7	ADJ92159	Adj92159 Human hai
251	57.5	20.1	292	7	ADJ92159	Adj92159 Human nov
252	57.5	20.1	477	7	ADC32665	Adc32665 Human nov
253	57.5	20.1	477	9	AE21141	Ae21141 Novel hum
254	57.5	20.1	658	5	AAW49759	Aaw49759 TNF-selec
255	57.5	20.1	739	9	AEA20333	Aea20333 Novel hum
256	57.5	20.1	751	7	ADC31546	Adc31546 Human nov
257	57.5	20.1	770	5	AE233388	Ae233388 Human int
258	57.5	20.1	770	7	ADC30933	Adc30933 Human nov
259	57.5	20.1	824	6	ADA55005	Ada55005 Human pro
260	57.5	20.1	838	6	ADN23792	Adn23792 Bacterial
261	57.5	20.1	858	8	ABM80296	Abm80296 Tumour-as
262	57.5	20.1	1511	4	ABB61693	Abb61693 Drosophil
263	56.5	20.0	2820	4	ABB63296	Abb63296 Drosophil
264	56.5	20.0	2820	8	ADO01056	Ado01056 Fruit fly
265	56	19.8	74	5	AB96689	Ab96689 Omega-con
266	56	19.8	126	4	ABG01157	Abg01157 Novel hum
267	56	19.8	268	8	ADT60022	Adt60022 Plant pol
268	56	19.8	337	4	ABB63629	Abb63629 Drosophil
269	56	19.8	337	4	AAU38954	Aau38954 Drosophil
270	56	19.8	337	7	ADC35844	Adc35844 Drosophil
271	56	19.8	760	4	ABB62427	Abb62427 Drosophil
272	56	19.8	2476	2	AAW67738	Aaw67738 Pig p105
273	56	19.8	2824	2	ADN22513	Adn22513 Bacterial
274	56	19.8	3597	5	AB809503	Ab809503 Human lam
275	56	19.8	3597	8	AD010047	Ad010047 Novel hum
276	56	19.8	3600	5	ABB09501	Abb09501 Human lam
277	56	19.8	3600	8	AD010043	Ad010043 Novel hum
278	55.5	19.6	225	4	ABB71511	Abb71511 Drosophil
279	55.5	19.6	339	7	ADB79814	Adb79814 Rat cathe
280	55.5	19.6	350	4	ABB68635	Abb68635 Drosophil
281	55.5	19.6	419	2	AAW11478	Aaw11478 Human vas
282	55.5	19.6	508	4	ABG22213	Abg22213 Novel hum
283	55.5	19.6	815	5	ABB93120	Abb93120 Herbicida
284	55.5	19.6	976	4	ABB11195	Abb11195 Human tra
285	55.5	19.6	1149	8	ADL33455	Adl33455 Festuca a
286	55.5	19.6	3650	8	ADM87254	Adm87254 Human pro
287	55.5	19.6	3695	8	ADN04478	Adn04478 Antipsori
288	55.5	19.6	3695	9	ADY25780	Ady25780 MRAC LAMA
289	55.5	19.6	3696	5	AAE17310	Aae17310 Human lam
290	55.5	19.6	3705	5	AAE17309	Aae17309 Human lam
291	55.5	19.6	5405	6	AAW14749	Aaw14749 IGG-Fc bi
292	55.5	19.6	5405	6	ABP55383	Abp55383 Human col
293	55.5	19.6	5405	7	ADL15023	Adl15023 Human IGG
294	55.5	19.6	5405	8	ADQ18828	Adq18828 Human sof
295	55.5	19.6	5405	9	ADV70227	Adv70227 Tumour-ass
296	55.5	19.6	7337	4	ABG22216	Abg22216 Novel hum
297	55	19.4	109	5	ABP09548	Abp09548 Human ORF
298	55	19.4	117	4	ABB63166	Abb63166 Drosophil
299	55	19.4	161	9	ADV69654	Adv69654 Human sol
300	55	19.4	328	2	AAR67628	Aar67628 Non-A Non

ALIGNMENTS

XX	RESULT 1	
FH	AEC02032	
FT	ID AEC02032 standard; peptide; 52 AA.	
FT	XX	
XX	AC AEC02032;	
AC	XX	
XX	DT 20-OCT-2005 (first entry)	
XX	XX	
XX	DE Amino acid sequence of an extracellular domain of BCMA.	
XX	XX	
XX	KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;	
XX	KW	

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PR 24-FEB-1999; 99US-0121485P.
XX (GEO ) GEN HOSPITAL CORP.
XX
XX Seed B, Ting A;
XX
XX WPI; 2000-558405/51.
XX
XX Identifying a modulator of gene expression for drug designing, by
PT contacting a compound library with a cell expressing an anti-cell death
PT gene and reporter gene, and determining alteration in reporter gene
PT expression.
XX
XX Claim 32; Fig 7A; 53pp; English.
XX
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
CC a necrosis factor (NF)-kB activator. The method of the invention is used
CC to identify compounds which modulate BCMA activity (and thus NF-kB
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to
CC the promoter, and then determining whether the expression of the reporter
CC gene is altered as a result of contact with library. The method is useful
CC for identifying polypeptides which increase or decrease gene expression
CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
CC preparing a pharmaceutical composition for treating cancer, apoptosis,
CC viral infections, inflammatory response, such as rheumatoid arthritis,
CC inflammatory bowel disease or septic shock. BCMA is useful for
CC identifying compounds that modulate NF-kB expression and thus for drug
CC designing
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 283; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 3
AA94001
ID AA94001 standard; protein; 184 AA.
XX
XX AA94001;
AC
XX
XX 20-OCT-2000 (first entry)
DT
XX
XX A human BCMA protein, a B cell protein related to TACI.
DE
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasms; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX Homo sapiens.
OS
XX
XX WO200040716-A2.
PN
XX
XX 13-JUL-2000.
PD
XX
XX 07-JAN-2000; 2000WO-US000396.
PF
XX
XX

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PR 07-JAN-1999; 99US-00226533.
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX
XX WPI; 2000-452538/39.
XX
XX N-FSDB; AA558559.
XX
XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX
XX Disclosure; Page 152; 175pp; English.
XX
XX The present sequence represents a human BCMA protein, a B cell protein
CC related to transmembrane activator and CAML-interactor (TACI) receptor.
CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
CC protein) receptor contain a cysteine rich domain, and are used for
CC inhibiting znf4 activity. Znf4 is a TNF ligand. They may also be used
CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC with activated or resting B lymphocytes, effector T-cells, or with
CC antibody production. The antibody production is associated with an
CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC asthma, bronchitis, emphysema, end stage renal failure,
CC glomerulonephritis, vasculitis, nephritis, light chain neuropathy,
CC neoplasms, multiple myelomas, lymphomas, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 283; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 4
AAE09241
ID AAE09241 standard; protein; 184 AA.
XX
XX AAE09241;
AC
XX
XX 19-NOV-2001 (first entry)
DT
XX
XX Human BCMA protein.
DE
XX
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX
XX Homo sapiens.
OS
XX
XX WO200160397-A1.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 28-NOV-2000; 2000WO-US032378.
PF
XX
XX 16-FEB-2000; 2000US-0182938P.
PR
XX
XX 22-AUG-2000; 2000US-0226986P.
XX
XX

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PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM,  
 PI Yan M;  
 XX WPI: 2001-541628/60.  
 DR N-PSDB; AAD15902.  
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists:  
 XX Example 2; Fig 2; 160pp; English.  
 XX The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TACI or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or  
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human BCMA protein  
 XX Sequence 184 AA;  
 SQ  
 Query Match 100.0%; Score 283; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSTPTPLTCQRYCNASVTNSVKG 51  
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSTPTPLTCQRYCNASVTNSVKG 51  
 RESULT 5  
 AAY71979  
 ID AAY71979 standard; protein; 184 AA.  
 AC AAY71979;  
 XX 28-MAR-2001 (first entry)  
 DT Human B cell maturation factor (BCMA) protein.  
 DE Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;  
 XX Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;  
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;  
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;  
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;  
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;  
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Domain 1..62  
 FT /label= Extracellular\_domain  
 FT  
 XX WO200068378-A1.  
 PN  
 XX 16-NOV-2000.  
 PD  
 XX 05-MAY-2000; 2000WO-US012266.  
 XX  
 XX 06-MAY-1999; 98US-0132892P.  
 PR  
 XX 01-MAY-2000; 2000US-0201012P.  
 XX  
 XX . (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;  
 PI  
 XX WPI: 2001-016094/02.  
 DR N-PSDB; AAD02125.  
 XX Isolated TALL-1 protein is used to identify compounds that regulate B  
 PT lymphocyte proliferation, used to treat B lymphocyte associated  
 PT autoimmune disorders.  
 XX Claim 37; Page 104-105; 112pp; English.  
 PS  
 XX The present invention relates to Tumour necrosis factor (TNF) and Apol-  
 CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,  
 CC proteins (including homologues), and their antibodies. The invention in  
 CC particular relates to methods for regulating the interaction between TALL  
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to  
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.  
 CC TALL-1 protein is useful for identifying compounds that regulate B  
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte  
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus  
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple  
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,  
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal  
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its  
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.  
 CC The present sequence is a human B cell maturation factor (BCMA) protein.  
 CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome  
 CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not  
 CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.  
 CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression  
 CC increases with B lymphocyte maturation  
 XX Sequence 184 AA;  
 SQ  
 Query Match 100.0%; Score 283; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSTPTPLTCQRYCNASVTNSVKG 51  
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSTPTPLTCQRYCNASVTNSVKG 51  
 RESULT 6  
 AAB60698  
 ID AAB60698 standard; protein; 184 AA.  
 XX AAB60698;  
 AC 22-MAY-2001 (first entry)  
 DT Human BAFF receptor (BAFF-R).  
 DE Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
 KW immune-related disorder; B-cell growth inhibitor; BCMA;  
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
 KW renal disorder; immunosuppressive disorder; HIV infection;  
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; gene therapy; cancer; tumour.  
 XX Homo sapiens.  
 OS  
 XX WO200112812-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 16-AUG-2000; 2000WO-US022507.  
 XX





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FT /note= "Cysteine rich region"
PN WO200266516-A2.
XX
XX 29-AUG-2002.
XX
XX 06-FEB-2002; 2002WO-US003500.
XX
XX 20-FEB-2001; 2001US-0270274P.
XX 12-APR-2001; 2001US-0283447P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Kindvogel W;
XX
XX WPI; 2002-723183/78.
XX N-PSDB; AAD46410.
XX
XX B-cell maturation antigen and transmembrane activator and calcium-
PT modulator and cyclophilin ligand-interactor, useful for treating
PT disorders e.g. inflammation or lymphoma.
XX
XX Disclosure; Page 63; 67pp; English.
XX
XX The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 5; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCORYCNASVTNSVKG 51
Db 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCORYCNASVTNSVKG 51

RESULT 11
AAE35216
XX AAE35216;
XX
XX 28-MAY-2003 (first entry)
XX
XX Human B-cell maturation receptor (BCMA) protein.
XX
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
XX TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
XX anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
XX glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
XX dermatological; neuroprotective; cyclophilin ligand-interactor; human;
XX autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
XX B-cell maturation receptor; BCMA; receptor.
XX
XX Homo sapiens.
XX
XX WO200294852-A2.
XX
XX 28-NOV-2002.
XX

/note= "Cysteine rich region"
PN WO200266516-A2.
XX
XX 29-AUG-2002.
XX
XX 06-FEB-2002; 2002WO-US003500.
XX
XX 20-FEB-2001; 2001US-0270274P.
XX 12-APR-2001; 2001US-0283447P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Kindvogel W;
XX
XX WPI; 2002-723183/78.
XX N-PSDB; AAD46410.
XX
XX B-cell maturation antigen and transmembrane activator and calcium-
PT modulator and cyclophilin ligand-interactor, useful for treating
PT disorders e.g. inflammation or lymphoma.
XX
XX Disclosure; Page 63; 67pp; English.
XX
XX The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 5; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCORYCNASVTNSVKG 51
Db 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCORYCNASVTNSVKG 51

RESULT 12
ADA49361
XX ADA49361 standard; protein; 184 AA.
XX
XX ADA49361;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human BCMA protein.
XX
XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;
XX antiinflammatory; antiarthritis; dermatological; antidiabetic;
XX neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;
XX vaccine; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; insulin dependent diabetes mellitus;
XX multiple sclerosis; myasthenia gravis; Grave's disease;
XX autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
XX Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
XX
XX Homo sapiens.
XX
XX WO2003035846-A2.
XX
XX 01-MAY-2003.
XX
XX 24-OCT-2002; 2002WO-US034376.
XX
XX 24-OCT-2001; 2001US-0345106P.
XX 14-JAN-2002; 2002US-0348962P.
XX 07-FEB-2002; 2002US-0354966P.
XX

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PR 13-AUG-2002; 2002US-0403364P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Zhang G, Shu H, Liu Y, Xu L;
XX
XX WPI; 2003-403345/38.
XX
XX N-PSDB; ADA9360.
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
XX
XX activity in mammal, has a modification in the region connecting beta
XX
XX strands D and E that reduces the biological activity of TALL-1
XX
XX antagonist.
XX
XX Claim 62; Page 613; 618pp; English.
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
XX
XX sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
XX
XX NO:2, by at least one modification in the region connecting  $\delta$ gr; strands
XX
XX D and E that reduces the biological activity of the TALL-1 antagonist as
XX
XX compared to wild-type TALL-1. A protein of the invention has
XX
XX immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
XX
XX dermatological, antidiabetic, neuroprotective, antithyroid, antipruritic,
XX
XX nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
XX
XX a vaccine. A protein of the invention is useful for inhibiting TALL-1
XX
XX biological activity in a mammal. TC is useful for treating autoimmune
XX
XX diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
XX
XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
XX
XX Grave's disease, autoimmune hemolytic anaemia, autoimmune
XX
XX thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
XX
XX acute rheumatic fever, post-streptococcal glomerulonephritis and
XX
XX polyarteritis nodosa. The present sequence represents human BCMA.
XX
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 6; Length 184;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX Qy 1 MLQWAGCQSQNEYFDSLHACIPQQLRCSSNTPTLTQRYCNASVTNSVKG 51
XX
XX Db 1 MLQWAGCQSQNEYFDSLHACIPQQLRCSSNTPTLTQRYCNASVTNSVKG 51
XX
XX
XX RESULT 13
XX
XX ABP60552
XX
XX ID ABP60552 standard; protein; 184 AA.
XX
XX AC ABP60552;
XX
XX XX
XX
XX 28-MAR-2003 (first entry)
XX
XX DE Human tumour necrosis factor BCMA.
XX
XX KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
XX
XX dermatological; immunosuppressive; antiinflammatory; antirheumatic;
XX
XX antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic;
XX
XX neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
XX
XX antipruritic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
XX
XX haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
XX
XX inflammatory disorder; proliferative disorder; single chain antibody;
XX
XX antibody; human; BCMA; tumour necrosis factor.
XX
XX OS Homo sapiens.
XX
XX XX
XX
XX WO200294192-A2.
XX
XX XX
XX
XX 28-NOV-2002.
XX
XX XX
XX
XX 22-MAY-2002; 2002WO-US016106.
XX
XX PF
XX
XX 24-MAY-2001; 2001US-0293100P.
XX
XX PR
XX
XX

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PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM;
XX
XX WPI; 2003-156740/15.
XX
XX Novel isolated antibody that immunospecifically binds tumor necrosis
XX
XX factor delta, useful for treating, preventing or ameliorating Non-
XX
XX Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
XX
XX syndrome.
XX
XX Disclosure; Page 222; 225pp; English.
XX
XX The invention relates to a novel antibody or its fragment, which
XX
XX immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
XX
XX The antibody of the invention has dermatological, immunosuppressive,
XX
XX antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
XX
XX antiallergic, antiashmatic, neuroprotective, ophthalmological,
XX
XX tuberculostatic, antidiabetic, antipruritic, anti-HIV,
XX
XX antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
XX
XX The antibody or its fragment are useful for treating, preventing or
XX
XX ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
XX
XX human, disease or disorder such as autoimmune disease, and graft versus
XX
XX host disease (GVHD). The autoimmune disease is systemic lupus
XX
XX erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
XX
XX is useful for detecting, diagnosing, prognosing, treating, preventing or
XX
XX ameliorating a disease or disorder associated with aberrant APRIL or
XX
XX APRIL receptor expression or aberrant function of APRIL or APRIL
XX
XX receptor. The disease or disorders includes autoimmune and inflammatory
XX
XX disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
XX
XX asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
XX
XX uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
XX
XX system, particularly B cell cancers, immune disorders such as myasthenia
XX
XX gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
XX
XX infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
XX
XX proliferative disorders (e.g. leukemia). The present sequence represents
XX
XX the tumour necrosis factor BCMA
XX
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 6; Length 184;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX Qy 1 MLQWAGCQSQNEYFDSLHACIPQQLRCSSNTPTLTQRYCNASVTNSVKG 51
XX
XX Db 1 MLQWAGCQSQNEYFDSLHACIPQQLRCSSNTPTLTQRYCNASVTNSVKG 51
XX
XX
XX RESULT 14
XX
XX ABP97717
XX
XX ID ABP97717 standard; protein; 184 AA.
XX
XX AC ABP97717;
XX
XX XX
XX
XX 28-MAY-2003 (first entry)
XX
XX DT Amino acid sequence of human BCMA receptor.
XX
XX DE Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX
XX TALL-1; April; systemic lupus erythematosus; BCMA.
XX
XX KW Homo sapiens.
XX
XX OS
XX
XX WO2003014294-A2.
XX
XX PN
XX
XX 20-FEB-2003.
XX
XX PD
XX
XX 24-JUL-2002; 2002WO-US023487.
XX
XX PF
XX
XX 03-AUG-2001; 2001US-0310114P.
XX
XX PR
XX
XX 30-APR-2002; 2002US-0377171P.
XX
XX PR
XX
XX

```

PA (GETH ) GENENTECH INC.  
XX  
PI Dixit V, Grewal I, Ridgway J, Yan M;  
XX  
DR WPI; 2003-256560/25.  
DR N-PSDB; AB268871.  
XX  
PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
PT preparing a composition for treating systemic lupus erythematosus.  
XX  
PS Disclosure; Fig 2; 153pp; English.  
XX  
CC The present sequence represents a human BCMA polypeptide. The  
CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are  
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April  
CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to  
CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for  
CC preparing a composition for treating systemic lupus erythematosus  
XX  
SQ Sequence 184 AA;  
  
Query Match 100.0%; Score 283; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQAGQCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
DB 1 MLQAGQCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
  
RESULT 15  
ADD67527  
ID ADD67527 standard; protein; 184 AA.  
XX  
AC ADD67527;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human Ly1732P protein SEQ ID NO:4.  
XX  
KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;  
KW vaccine; immunotherapy; cancer; multiple myeloma cell;  
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;  
KW human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003062401-A2.  
XX  
PD 31-JUL-2003.  
XX  
PF 22-JAN-2003; 2003WO-US002353.  
XX  
PR 22-JAN-2002; 2002US-00057475.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;  
PI Carter L, Mcneill PD;  
XX  
DR WPI; 2003-598749/56.  
DR N-PSDB; ADD67526.  
XX  
PT New hematological malignancy-related genes and polypeptides, useful for  
PT screening anti-cancer agents, and generating antibodies or  
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic  
PT lymphocytic leukemia.  
XX  
PS Claim 9; SEQ ID NO 4; 307pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I), which is  
CC overexpressed in haematological malignancies, and which encodes a  
CC polypeptide or an immunogenic fragment of the polypeptide. Also  
CC  
CC described: (1) an isolated polypeptide; (2) an expression vector  
CC comprising (I) operably linked to an expression control sequence; (3) a  
CC host cell comprising an expression vector; (4) an isolated antibody that  
CC specifically binds to the polypeptide or its immunogenic fragment; and  
CC (5) immunoconjugates comprising the antibody above, or an antibody that  
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded  
CC by (I). (I) has cytostatic and immunostimulant activities, and can be  
CC used in vaccines and immunotherapy. The immunoconjugates are useful in  
CC the manufacture of a medicament, particularly as active ingredients in a  
CC composition for treating cancer, e.g. multiple myeloma cell, chronic  
CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,  
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.  
CC The polynucleotide (I) or polypeptide can be used for screening anti-  
CC cancer agents, and generating antibodies or immunoconjugates for treating  
CC or preventing the above-mentioned diseases. The polynucleotide,  
CC polypeptide or antibody can be used for detecting, diagnosing or  
CC prognosticating the haematological malignancies described above. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 184 AA;  
  
Query Match 100.0%; Score 283; DB 7; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQAGQCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
DB 1 MLQAGQCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
  
RESULT 16  
ADG43715  
ID ADG43715 standard; protein; 184 AA.  
XX  
AC ADG43715;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human B-cell maturation antigen SEQ ID NO:1.  
XX  
KW human; neurodegenerative immunological disorder; demyelination;  
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;  
KW BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003072713-A2.  
XX  
PD 04-SEP-2003.  
XX  
PF 21-FEB-2003; 2003WO-US005147.  
XX  
PR 21-FEB-2002; 2002US-0358427P.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Kalled SL, Reid H;  
XX  
DR WPI; 2003-721758/68.  
DR N-PSDB; ADG43716.  
XX  
PT Treating a neurodegenerative immunological disorder, e.g. demyelination  
PT or inflammation in a mammal comprises administering a B-cell maturation  
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.  
XX  
PS Claim 8; Page 68-69; 72pp; English.  
XX  
CC The invention relates to a novel method for treating a neurodegenerative  
CC immunological disorder, demyelination or Central Nervous System (CNS)  
CC inflammation in a mammal. The method comprises administering B-cell  
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand  
CC (the mammal has or is at risk of developing multiple sclerosis). The

CC method of the invention has neuroprotective, nootropic, and  
CC antiinflammatory activity, and may have a use in gene therapy. The  
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative  
CC immunological disorder such as multiple sclerosis, demyelination or CNS  
CC inflammation. The present sequence represents human BCMA.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 7; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
|||||

RESULT 17

ADK00756  
ID ADK00756 standard; protein; 184 AA.

XX AC ADK00756;

XX DT 06-MAY-2004 (first entry)

XX DE Native human BCMA.

XX KW CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;  
KW Dermatological; Immunosuppressive; Antiirheumatic; Antiarthritic;  
KW Antidiabetic; Neuroprotective; Antialsthmatic; Antiallergic; Anti-HIV;  
KW Antibacterial; antiparasitic; systemic lupus erythematosus;  
KW diabetes mellitus; AIDS; BCMA.

XX OS Homo sapiens.

XX PN WO2004011611-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023421.

XX PR 25-JUL-2002; 2002US-0398530P.

XX PA (GETH ) GENENTECH INC.

XX PI Chuntharapai A, Grewal I, Kim KJ, Yan M;

XX DR WPI; 2004-143841/14.

XX DR N-PSDB; ADK00755.

XX PT New anti-TACI receptor monoclonal antibody, useful for diagnosing and  
PT treating pathological conditions associated with tumor necrosis factor,  
PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or  
PT psoriasis.

XX PS Disclosure; SEQ ID NO 6; 110pp; English.

XX CC The present invention relates to an isolated monoclonal antibody which  
CC binds to a transmembrane activator of and CAML interactor (TACI)  
CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI  
CC polypeptide biological activity in mammalian cells, or for diagnosing and  
CC treating pathological conditions associated with TNF and TNF receptor-  
CC related molecules, e.g. cancer or immune-related disease, such as  
CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,  
CC systemic vasculitis, diabetes mellitus, Crohn's disease,  
CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or  
CC infectious diseases including AIDS, hepatitis infection, bacterial  
CC infection, fungal infection, protozoal infection and parasitic infection.  
CC The present sequence represents native human BCMA.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 8; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
|||||

RESULT 18

ADQ94442  
ID ADQ94442 standard; protein; 184 AA.

XX AC ADQ94442;

XX DT 07-OCT-2004 (first entry)

XX DE Neurokine-alpha, BCMA.

XX KW neurokine-alpha; chelator; B-lymphocyte stimulator; BlyS; TALL-1; THANK;  
KW BAFF; neurokine-alpha receptor; complex; metal ion; radiotherapy;  
KW B-cell mediated disease; non-Hodgkin's lymphoma;  
KW chronic lymphocytic leukaemia; multiple myeloma;  
KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;  
KW Crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis;  
KW asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte;  
KW B cell; cancerous cell; metastasis; lymphatic system.

XX OS Homo sapiens.

XX PN WO2004058309-A1.

XX PD 15-JUL-2004.

XX PF 22-DEC-2003; 2003WO-US040979.

XX PR 23-DEC-2002; 2002US-0435262P.

XX PR 02-MAY-2003; 2003US-0467198P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Parmelee D, Yeh R, Galperina O, Hilbert D, Rosen CA;

XX DR WPI; 2004-553134/53.

XX DR N-PSDB; ADQ94441.

XX DR GENBANK; NM\_001192.

XX PT Neurokine-alpha conjugate useful for targeting complexed metal ion to  
PT cells expressing receptor (predominantly lymphoid) for radiotherapy  
PT treatment of, for example, non-Hodgkin's lymphoma comprises neurokine-  
PT alpha protein and chelator.

XX PS Disclosure; SEQ ID NO 9; 228pp; English.

XX CC This sequence represents neurokine-alpha, BCMA, which may be used in the  
CC protein conjugate of the invention. The neurokine-alpha protein  
CC conjugate comprises neurokine-alpha protein and chelator, where the  
CC neurokine-alpha protein (also known as B-lymphocyte stimulator (BlyS),  
CC TALL-1, THANK and BAFF) is capable of binding neurokine-alpha receptor.  
CC The and is selected from full length or mature neurokine-alpha protein. The  
CC protein conjugate of the invention is useful in a complex with a metal  
CC ion associated with the chelator which is useful for administering  
CC radiotherapy to a subject such as human who is in need of radiotherapy,  
CC which involves administering the complex to the subject, where it is  
CC administered as an injectable solution, and the subject has a B-cell  
CC mediated disease. The subject has a condition chosen from non-Hodgkin's  
CC lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus  
CC erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease,  
CC diabetes, Wegener's granulomatosis, myasthenia gravis and asthma,  
CC preferably non-Hodgkin's lymphoma. The complex is useful for treating  
CC cancer, which involves administering it to a subject having cancer, where  
CC a cell of the cancer expresses a neurokine-alpha receptor on its  
CC surface. The cancer is a B cell cancer, which is chosen from non-  
CC Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia.

CC The complex is also useful for treating an autoimmune disease or  
CC disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis  
CC and Sjogren's syndrome. The complex may also be used for diagnostic  
CC imaging. A composition comprising the protein conjugate or the complex is  
CC useful for killing a cell chosen from a cell bearing a neurokinine-alpha  
CC receptor, and a cell in close proximity to a cell bearing neurokinine-  
CC alpha receptor, which involves contacting the cell with the composition  
CC to kill the cell. The cell is lymphocyte, B cell or cancerous cell that  
CC has metastasised into the lymphatic system.

XX  
SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 8; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||

RESULT 19  
ADP56014  
ID ADP56014 standard; protein; 184 AA.  
XX  
AC ADP56014;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human PRO protein sequence SEQ ID NO:1990.  
XX  
KW human; PRO; immune related disease; inflammatory immune response;  
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;  
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;  
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
KW virucide; gene therapy.

XX  
OS Homo sapiens.  
XX  
PN WO2004039956-A2.  
XX  
PD 13-MAY-2004.  
XX  
PF 28-OCT-2003; 2003WO-US034381.  
XX  
PR 29-OCT-2002; 2002US-0422472P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
PI Wood WI, Wu TD;  
XX  
DR WPI: 2004-376182/35.  
DR N-PSDB; ADP56013.  
XX

New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
PT and treating an immune related disease, e.g. systemic lupus  
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
PT stimulating an immune response.

XX  
PS Claim 1; SEQ ID NO 1990; 3009pp; English.

XX  
CC The present invention describes an isolated PRO nucleic acid (I). Also  
CC described: (1) a vector comprising (I); (2) a host cell comprising the  
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
CC antibody which specifically binds to a polypeptide of (4); (7) a  
CC composition of matter comprising a polypeptide of (4), an agonist or  
CC antagonist of the polypeptide or an antibody that binds to the  
CC polypeptide in combination with a carrier; (8) an article of manufacture

CC comprising a container, a label on the container and a composition of  
CC matter of (7); (9) a method of treating an immune related disease in a  
CC mammal; (10) a method for determining the presence of a PRO polypeptide  
CC in a sample suspected of having the polypeptide; (11) a method of  
CC diagnosing an immune related disease or an inflammatory immune response  
CC in mammal; (12) a method of identifying a compound that inhibits or  
CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
CC ; and (13) a method of stimulating the immune response in a mammal. The  
CC PRO sequences have antiallergic, antianaemic, antiarthritic,  
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,  
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,  
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
CC virucide activities, and can be used in gene therapy. The nucleic acid  
CC (I) and the encoded polypeptides, compositions, kits and methods are  
CC useful in diagnosing and treating an immune related disease and in  
CC stimulating an immune response. The present sequence represents a human  
CC PRO protein from the present invention.

XX  
SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 8; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||

RESULT 20  
ADW03432  
ID ADW03432 standard; protein; 184 AA.  
XX  
AC ADW03432;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Human BCMA protein amino acid sequence.  
XX  
KW B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;  
KW non-hodgkin lymphoma; hodgkins disease; cytostatic;  
KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;  
KW antiarthritic; antirheumatic; systemic lupus erythematosus;  
KW Wegener granulomatosis; antiallergic; antiinflammatory; vasotropic;  
KW inflammatory bowel disease; gastrointestinal-gen.;  
KW idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;  
KW asthma; antiasthmatic; psoriasis; antipsoriatic; myasthenia gravis;  
KW muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;  
KW glomerulonephritis; nephrotropic; BCMA.

XX  
OS Homo sapiens.  
XX  
PN WO2005000351-A2.  
XX  
PD 06-JAN-2005.  
XX  
PF 04-JUN-2004; 2004WO-US017693.  
XX  
PR 05-JUN-2003; 2003US-0476414P.  
PR 05-JUN-2003; 2003US-0476481P.  
PR 06-JUN-2003; 2003US-0476531P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Chan A, Gong Q, Martin F;  
XX  
XX WPI: 2005-058069/06.  
XX N-PSDB; ADW03431.  
XX

Depleting B cells from a mixed population of cells by contacting the  
PT cells with a Blys antagonist and a CD20 binding antibody, useful for  
PT treating B cell malignancies and autoimmune disorders.



CC cell proliferative disorder. Also disclosed are anti-tumor antigens of  
CC hematopoietic origin (TAHO) polypeptides, encoding nucleic acids, methods of  
CC oligopeptides, vectors, host cells and antibodies used in the methods of  
CC the invention. The methods and compositions of the present invention are  
CC useful for treating hematopoietic and malignant tumors in mammals. This  
CC is the amino acid sequence of tumor antigen of hematopoietic origin  
CC TAO23.  
XX  
SQ Sequence 184 AA;  
  
Query Match 100.0%; Score 283; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
  
RESULT 23  
ASC02031  
ID AEC02031 standard; protein; 184 AA.  
XX  
AC AEC02031;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Amino acid sequence of a BCMA protein.  
XX  
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;  
KW B-cell maturation antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO2005075511-A1.  
XX  
PD 18-AUG-2005.  
XX  
PF 04-AUG-2004; 2004WO-US025247.  
XX  
PR 29-JAN-2004; 2004US-0540271P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Kelley RF, Patel D;  
XX  
DR WPI; 2005-555932/56.  
XX  
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
PS Disclosure; SEQ ID NO 20; 140pp; English.  
XX  
CC The specification describes polypeptides that bind April or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC scleroma; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents a BCMA protein.  
XX  
SQ Sequence 184 AA;  
  
Query Match 100.0%; Score 283; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51

DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51  
  
RESULT 24  
AAB60699  
ID AAB60699 standard; protein; 302 AA.  
XX  
AC AAB60699;  
XX  
DT 11-SEP-2003 (revised)  
DT 22-MAY-2001 (first entry)  
XX  
DE Mouse IgG signal/human BAFF-R/human Igg Fc fusion protein, BAFF-R-Fc.  
XX  
KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
KW immune-related disorder; B-cell growth inhibitor;  
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
KW renal disorder; immunosuppressive disorder; HIV infection;  
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
KW lymphoma; gene therapy; cancer; tumour; Igg Fc; fusion construct.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
PN WO200112812-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 16-AUG-2000; 2000WO-US022507.  
XX  
PR 17-AUG-1999; 99US-0149378P.  
PR 11-FEB-2000; 2000US-0181684P.  
PR 18-FEB-2000; 2000US-0183536P.  
XX  
PA (BIOJ ) BIOGEN INC.  
PA (APOT-) APOTEC R & D SA.  
XX  
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
PI Thompson J;  
XX  
DR WPI; 2001-202866/20.  
DR N-PSDB; AAF59999.  
XX  
PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
XX  
PS Example 4; Fig 2; 59pp; English.  
XX  
CC The invention relates to the use of a BAFF receptor (BAFF-R, also known  
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
CC agent, and also plays a role in the development of hypertension and  
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
CC be used in the treatment of immunosuppressive disorders and HIV  
CC infection, and in patients undergoing organ transplantation. The BAFF-R  
CC proteins or BAFF-R specific antibodies may be used for treating,  
CC suppressing or altering an immune response involving a signalling pathway  
CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R  
CC inhibits B-cell growth and maturation it is useful for treating diseases  
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding

CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,  
 CC autoimmune disorders and inherited B-cell-associated disorders. The  
 CC present sequence represents the BAPF-R fusion protein BAPF-R-Fc,  
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human  
 CC BAPF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to  
 CC standardise OS field)

XX  
 PS Sequence 302 AA;  
 CC Query Match 100.0%; Score 283; DB 4; Length 302;  
 CC Best Local Similarity 100.0%; Pred. No. 2.4e-25;  
 CC Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51  
 DB 24 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 74

RESULT 25  
 AAE00507  
 ID AAE00507 standard; protein; 302 AA.  
 AC AAE00507;  
 DT 11-SEP-2003 (revised)  
 DT 31-JUL-2001 (first entry)  
 DE Human BCMA-Immunoglobulin G Fc region fusion construct.

XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;  
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;  
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;  
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;  
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;  
 KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;  
 KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;  
 KW immunoglobulin G; IgG; Fc region.

XX Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.

XX  
 FH Key Location/Qualifiers  
 FT Protein 1..22 /label= Signal\_peptide  
 FT /note= "Derived from murine Ig kappa sequence"  
 FT Protein 23..302  
 FT /label= Mature\_human\_BCMA\_IgG\_Fc\_fusion\_protein  
 FT Region 23..75 /note= "Derived from human BCMA protein"  
 FT Domain 24..302 /label= Cysteine\_rich\_domain  
 FT /note= "Derived from human BCMA"  
 FT Region 76..302  
 FT /note= "Derived from human IgG Fc region"

XX WO200124811-A1.  
 PN 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US027579.  
 XX 06-OCT-1999; 99US-0157933P.  
 PR 11-FEB-2000; 2000US-0181807P.  
 PR 30-JUN-2000; 2000US-0215688P.  
 XX (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTEC R & D SA.  
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
 XX WPI; 2001-266242/27.  
 DR N-PSDB; AAD03847.

XX Treating a mammal for a condition associated with undesired cell  
 PT proliferation such as cancer or carcinoma, comprises administering a  
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
 PT antagonist.

XX  
 PS Example 1; Fig 3B; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition  
 CC associated with undesired cell proliferation such as cancer or carcinoma.  
 CC The method involves administering a composition comprising A  
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell  
 CC maturation protein (BCM or BCMA) antagonist that antagonises the  
 CC interaction between APRIL and its cognate receptor(s). This method is  
 CC useful for treating undesired cell proliferation such as cancer or  
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,  
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated  
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's  
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular  
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
 CC immunosuppressive diseases, organ transplantation, inflammation and human  
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering  
 CC an immune response involving a signalling pathway between APRIL-R and its  
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
 CC is a fusion construct containing human APRIL-R also referred as BCMA or  
 CC BCM protein, Fc region of human immunoglobulin G (IgG) and a signal  
 CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to  
 CC standardise OS field)

XX  
 SQ Sequence 302 AA;  
 CC Query Match 100.0%; Score 283; DB 4; Length 302;  
 CC Best Local Similarity 100.0%; Pred. No. 2.4e-25;  
 CC Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 51  
 DB 24 MLOMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASTNSVKG 74

RESULT 26  
 ADG43717  
 ID ADG43717 standard; protein; 302 AA.  
 AC ADG43717;  
 DT 26-FEB-2004 (first entry)  
 DE Human B-cell maturation antigen-Fc SEQ ID NO:3.  
 XX human; neurodegenerative immunological disorder; demyelination;  
 KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;  
 KW BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;  
 KW gene therapy; mouse.  
 XX Chimeric.  
 OS Homo sapiens.  
 OS Mus sp.

XX  
 FH Key Location/Qualifiers  
 FT Region 1..23 /note= "Murine IgGkappa signal sequence"  
 FT Region 24..74 /note= "Human BCMA extracellular domain"  
 FT Region 75..302 /note= "Human Ig heavy chain Fc region"

XX WO2003072713-A2.  
 PN 04-SEP-2003.  
 XX 21-FEB-2003; 2003WO-US005147.  
 XX

```
PR 21-FEB-2002; 2002US-0358427P.
XX (BIOJ ) BIOGEN INC.
PA Kalled SL, Reid H;
XX WPI; 2003-721758/68.
DR N-PSDB; ADG43718.
XX
PT Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
PS Claim 12; Page 70-71; 72pp; English.
XX
CC The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, nootropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 302 AA;
Query Match 100.0%; Score 283; DB 7; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 24 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 74
RESULT 27
ABR40082
ID ABR40082 standard; protein; 184 AA.
XX
AC ABR40082;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human Genoxit.
XX
KW Human; Genoxit; anorectic; antilipaeamic; antiarteriosclerotic; cardiant;
KW antidiabetic; hypotensive; ophthalmological; neuroprotective;
KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
KW Type III transmembrane protein; insulin resistance; atherosclerosis;
KW atheronotous disease; heart disease; hypertension; stroke; syndrome X;
KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..54
FT /label= Extracellular_domain
FT Misc-difference 3
FT /label= Gln, Lys
FT Domain 55..77
FT /label= Transmembrane_domain
FT Domain 78..184
FT /label= Intracellular_domain
XX
PN WO2003013582-A1.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-IB003498.
XX
```

```
PR 06-AUG-2001; 2001US-0310754P.
XX (GEST ) GENSET SA.
PA Lucas J, Dialynas D, Briggs K;
XX WPI; 2003-268160/26.
DR N-PSDB; ACC00340.
XX
PT New use of agonist or antagonist of Genoxit activity for preventing or
PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
PT atherosclerosis.
XX
PS Disclosure; Page 32; 35pp; English.
XX
CC The present invention relates to the use of an agonist or antagonist of
CC Genoxit activity for preventing or treating obesity. Genoxit is a member
CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
CC transmembrane protein. The agonists or antagonists of the invention are
CC useful for treating or preventing obesity-related diseases or disorders,
CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
CC complications, e.g. microangiopathic lesions, ocular lesions,
CC retinopathy, neuropathy and renal lesions
XX
SQ Sequence 184 AA;
Query Match 97.9%; Score 277; DB 6; Length 184;
Best Local Similarity 98.0%; Pred. No. 7.3e-25;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 1 MLXWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
RESULT 28
ABG95060
ID ABG95060 standard; protein; 288 AA.
XX
AC ABG95060;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human translocation (4; 16)(q26; p13) protein.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006518.
XX
PR 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
DR N-PSDB; ABS73235.
```





PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
XX 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
XX Theill LE, Yu G;  
XX WPI; 2002-066686/09.  
XX  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10A; 94pp; English.  
XX  
XX The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human BCMA protein  
XX  
SQ Sequence 181 AA;  
Query Match 95.1%; Score 269; DB 5; Length 181;  
Best Local Similarity 100.0%; Pred. No. 6.5e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MAGQCSQNEYFDSLHACIPQLRCSNTPTLTQRYCNASVTNSVKG 51  
|||  
Db 1 MAGQCSQNEYFDSLHACIPQLRCSNTPTLTQRYCNASVTNSVKG 48  
|||  
RESULT 31  
AAE15488  
ID AAE15488 standard; protein; 283 AA.  
XX  
AC AAE15488;  
XX  
XX 12-MAR-2002 (first entry)  
XX  
XX Human BCMA-immunoglobulin Fc region fusion protein.  
XX  
XX Human; transmembrane activator and intracellular CAML interactor; TACI;  
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis; fusion protein.  
OS Homo sapiens.  
XX  
XX

PN WO200187979-A2.  
XX  
PD 22-NOV-2001.  
XX  
XX 14-MAY-2001; 2001WO-US015567.  
PF  
XX 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Theill LE, Yu G;  
XX WPI; 2002-066686/09.  
XX  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10B; 94pp; English.  
XX  
XX The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human BCMA protein-immunoglobulin Fc region fusion protein  
XX  
SQ Sequence 283 AA;  
Query Match 95.1%; Score 269; DB 5; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MAGQCSQNEYFDSLHACIPQLRCSNTPTLTQRYCNASVTNSVKG 51  
|||  
Db 1 MAGQCSQNEYFDSLHACIPQLRCSNTPTLTQRYCNASVTNSVKG 48  
|||  
RESULT 32  
AEC02042  
ID AEC02042 standard; protein; 296 AA.  
XX  
AC AEC02042;  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Amino acid sequence of a BCMA-Fc fusion protein.  
XX  
XX APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;  
KW B-cell maturation antigen; Fc.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX  
XX WO2005075511-A1.  
XX  
XX

PD 18-AUG-2005.  
 XX  
 PF 04-AUG-2004; 2004WO-US025247.  
 XX  
 PR 29-JAN-2004; 2004US-0540271P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Kelley RF, Patel D;  
 XX  
 DR WPI; 2005-555932/56.  
 XX  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX  
 PS Example 6; SEQ ID NO 31; 140pp; English.  
 XX  
 CC The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis factor (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC scleroma; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents a BCMA-Fc fusion protein, where 122 of BCMA is changed to Lys.  
 XX  
 XX Sequence 296 AA;  
 SQ  
 Query Match 90.8%; Score 257; DB 9; Length 296;  
 Best Local Similarity 97.9%; Pred. No. 2.9e-22;  
 Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 AGCQSQNEYFDSLHACIPQLRCSNTPLTTCORYCNASVTSVKG 51  
 DB 18 AGCQSQNEYFDSLHACKPQLRCSNTPLTTCORYCNASVTSVKG 64  
 RESULT 33  
 AAE15501  
 ID AAE15501 standard; peptide; 58 AA.  
 XX  
 AC AAE15501;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human B cell maturation protein cysteine rich extracellular region.  
 XX  
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;  
 KW cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;  
 KW lymphoproliferative disorder; tumor; lung; gastrointestinal; pancreatic;  
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
 KW rheumatoid arthritis; atherosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200187979-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 14-MAY-2001; 2001WO-US015567.  
 XX  
 PR 12-MAY-2000; 2000US-0204039P.  
 PR 27-JUN-2000; 2000US-0214591P.  
 PR 14-MAY-2001; 2001US-00214591.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI  
 XX  
 DR  
 XX  
 PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as

PI Theill LE, Yu G;  
 XX  
 DR WPI; 2002-066686/09.  
 XX  
 PT Inhibiting activity of B cell maturation protein and/or transmembrane  
 PT activator and intracellular cyclophilin ligand interactor, by  
 PT administering a binding partner for APRIL, a tumor necrosis factor family  
 PT ligand.  
 XX  
 PS Disclosure; Fig 13; 94pp; English.  
 XX  
 CC The invention relates to a method for inhibiting TACI (transmembrane  
 CC activator and intracellular CAML interactor) and/or B cell maturation  
 CC protein (BCMA) activity in a mammal. The method comprises administering a  
 CC specific binding partner for APRIL (G70, a tumor necrosis factor-TNF  
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
 CC BCMA extracellular consensus sequence, but not the extracellular region  
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
 CC lymphoproliferative disorders, one or more solid tumors such as lung,  
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
 CC antagonists are useful for treating inflammation and immune function  
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
 CC disease), drug and insect sting allergy, inflammatory bowel disease  
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
 CC with leucocyte infiltration of the skin or organs. The present sequence  
 CC is human BCMA cysteine-rich extracellular region  
 XX  
 SQ Sequence 58 AA;  
 Query Match 88.0%; Score 249; DB 5; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-22;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 CSQNEYFDSLHACIPQLRCSNTPLTTCORYCNASVTSVKG 51  
 DB 1 CSQNEYFDSLHACIPQLRCSNTPLTTCORYCNASVTSVKG 44  
 RESULT 34  
 ADZ67761  
 ID ADZ67761 standard; protein; 40 AA.  
 XX  
 AC ADZ67761;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Human tumor necrosis factor receptor BCMA Cys-rich domain.  
 XX  
 KW Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;  
 KW cytosolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005037865-A2.  
 XX  
 PD 28-APR-2005.  
 XX  
 PF 18-OCT-2004; 2004WO-US034375.  
 XX  
 PR 16-OCT-2003; 2003US-0511698P.  
 PR 18-OCT-2004; 2004US-0619552P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;  
 XX  
 DR WPI; 2005-315682/32.  
 XX  
 PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as

PT detecting ligands, and for modulating tumor growth, metastasis and  
PT immunity, such as separating resting from stimulated immune cells.  
XX  
PS Disclosure; SEQ ID NO 9; 132pp; English.  
XX  
CC The invention provides novel tumor necrosis factor receptor ztnfr14  
CC polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors  
CC and antibodies. Ztnfr14 polynucleotides are used in claimed methods for  
CC detecting a genetic abnormality in a patient and for detecting a cancer  
CC in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a  
CC toxin, is used in a claimed method of killing cancer cells. ztnfr14  
CC polypeptides can be used to detect ligands, agonists and antagonists. The  
CC polypeptides, polynucleotides and antibodies may also be used in methods  
CC that modulate tumor growth, metastasis, and immunity such as separating  
CC resting from stimulated immune cells. The present sequence is that of the  
CC Cys-rich domain of human TNFR BCMA ADZ67760. This sequence was compared  
CC with that of ztnfr14 in the identification of ztnfr14 as a member of the  
CC TNFR family.  
XX  
XX Sequence 40 AA;  
SQ

Query Match 81.3%; Score 230; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 5.9e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASV 45  
DB 1 GGCQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASV 40  
|||||

RESULT 35  
AEC02033  
ID AEC02033 standard; peptide; 38 AA.  
XX  
AC AEC02033;  
DT 20-OCT-2005 (first entry)  
XX  
DE Amino acid sequence of an extracellular domain of BCMA.  
XX  
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic;  
KW B-cell maturation antigen; BCMA.  
XX  
XX Synthetic.  
OS  
XX  
XX WO2005075511-A1.  
XX  
XX 18-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
PS Disclosure; SEQ ID NO 22; 140pp; English.  
XX  
CC The specification describes polypeptides that bind April or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

CC scleroma; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents an extracellular domain of BCMA.  
XX  
SQ Sequence 38 AA;  
XX

Query Match 76.0%; Score 215; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 3.4e-18;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SONEYFDSLHACIPQLRCSSNTPPLTCORYCNASVT 46  
DB 1 SONEYFDSLHACIPQLRCSSNTPPLTCORYCNASVT 38  
|||||

RESULT 36  
AAB60700  
ID AAB60700 standard; protein; 157 AA.  
XX  
AC AAB60700;  
XX  
XX 22-MAY-2001 (first entry)  
XX  
XX Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.  
XX  
KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;  
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
KW renal disorder; immunosuppressive disorder; HIV infection;  
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.  
XX  
OS Homo sapiens.  
XX  
XX WO200112812-A2.  
XX  
XX 22-FEB-2001.  
XX  
XX 16-AUG-2000; 2000WO-US022507.  
XX  
XX 17-AUG-1999; 99US-0149378P.  
XX  
XX 11-FEB-2000; 2000US-0181684P.  
XX  
XX 18-FEB-2000; 2000US-0183536P.  
XX  
XX (BIOJ ) BIOGEN INC.  
XX  
XX (APOT-) APOTEC R & D SA.  
XX  
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
XX Thompson J;  
XX  
XX WPI; 2001-202866/20.  
XX  
XX N-PSDB; AAF60000.  
XX  
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
XX  
XX Example 1; Fig 3; 59pp; English.  
XX  
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
CC agent, and also plays a role in the development of hypertension and  
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
CC be used in the treatment of immunosuppressive disorders and HIV



XX The invention relates to a novel TALL-1 antagonist protein, comprising a  
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID  
CC NO:2, by at least one modification in the region connecting abgr; strands  
CC D and E that reduces the biological activity of the TALL-1 antagonist as  
CC compared to wild-type TALL-1. A protein of the invention has  
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,  
CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,  
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in  
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1  
CC biological activity in a mammal. TC is useful for treating autoimmune  
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin  
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,  
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune  
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,  
CC acute rheumatic fever, post-streptococcal glomerulonephritis and  
CC polyarteritis nodosa. The present sequence represents a cysteine rich  
CC domain (CRD) module of human BCMA.  
XX  
SQ Sequence 34 AA;  
  
Query Match 71.0%; Score 201; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
DB 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
|||||  
  
RESULT 39  
AEC02026  
ID AEC02026 standard; peptide; 34 AA.  
XX  
AC AEC02026;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Formula II derived polypeptide E that binds BAFF.  
XX  
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
OS Synthetic.  
XX  
PN WO2005075511-A1.  
XX  
PD 18-AUG-2005.  
XX  
PF 04-AUG-2004; 2004WO-US025247.  
XX  
PR 29-JAN-2004; 2004US-0540271P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Kelley RF, Patel D;  
XX  
DR WPI; 2005-555932/56.  
XX  
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
PS Claim 13; SEQ ID NO 15; 140pp; English.  
XX  
PR 29-JAN-2004; 2004US-0540271P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Kelley RF, Patel D;  
XX  
DR WPI; 2005-555932/56.  
XX  
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
PS Claim 13; SEQ ID NO 15; 140pp; English.  
XX  
CC The specification describes polypeptides that bind April or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC sclerosis, or T-cell mediated disease such as graft rejection, graft

CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents a polypeptide of the invention, derived from formula II (see  
CC AEC02021), that that bind BAFF.  
XX  
SQ Sequence 34 AA;  
  
Query Match 69.6%; Score 197; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 4.2e-16;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
DB 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
|||||  
  
RESULT 40  
AEC02027  
ID AEC02027 standard; peptide; 34 AA.  
XX  
AC AEC02027;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Formula II derived polypeptide F that binds BAFF.  
XX  
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
OS Synthetic.  
XX  
PN WO2005075511-A1.  
XX  
PD 18-AUG-2005.  
XX  
PF 04-AUG-2004; 2004WO-US025247.  
XX  
PR 29-JAN-2004; 2004US-0540271P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Kelley RF, Patel D;  
XX  
DR WPI; 2005-555932/56.  
XX  
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
PS Claim 13; SEQ ID NO 16; 140pp; English.  
XX  
CC The specification describes polypeptides that bind April or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC sclerosis, or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents a polypeptide of the invention, derived from formula II (see  
CC AEC02021), that that bind BAFF.  
XX  
SQ Sequence 34 AA;  
  
Query Match 69.3%; Score 196; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 5.6e-16;  
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
DB 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
|||||

```

RESULT 41
AEC02028
ID AEC02028 standard; peptide; 34 AA.
XX AC AEC02028;
XX DT 20-OCT-2005 (first entry)
XX DE Formula II derived polypeptide G that binds BAFF.
XX KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX OS Synthetic.
XX PN WO2005075511-A1.
XX PD 18-AUG-2005.
XX PF 04-AUG-2004; 2004WO-US025247.
XX PR 29-JAN-2004; 2004US-0540271P.
XX PA (GETH ) GENENTECH INC.
XX PI Kelley RF, Patel D;
XX DR WPI; 2005-555932/56.
XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
    for treating immune-related disease, cancer or T-cell mediated disease
    such as graft rejection, graft versus host disease (GVHD) and
    inflammation.
XX PS Claim 7; SEQ ID NO 6; 140pp; English.
XX CC The specification describes polypeptides that bind APRIL or BAFF. The
    polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
    (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
    polypeptides of the invention are useful for treating immune-related
    diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
    lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
    sclerosis; or T-cell mediated disease such as graft rejection, graft
    versus host disease (GVHD) and inflammation. The present sequence
    represents a polypeptide of the invention that binds APRIL, derived from
    AEC02012.
XX SQ Sequence 34 AA;
    Query Match 68.6%; Score 194; DB 9; Length 34;
    Best Local Similarity 97.1%; Pred. No. 9.7e-16;
    Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 42
AEC02025
ID AEC02025 standard; peptide; 34 AA.
XX AC AEC02025;
XX DT 20-OCT-2005 (first entry)
XX DE Formula II derived polypeptide D that binds BAFF.
XX KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX OS Synthetic.
XX PN WO2005075511-A1.
XX PD 18-AUG-2005.
XX PF 04-AUG-2004; 2004WO-US025247.
XX PR 29-JAN-2004; 2004US-0540271P.
XX PA (GETH ) GENENTECH INC.
XX PI Kelley RF, Patel D;
XX DR WPI; 2005-555932/56.
XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
    for treating immune-related disease, cancer or T-cell mediated disease
    such as graft rejection, graft versus host disease (GVHD) and
    inflammation.
XX PS Claim 13; SEQ ID NO 17; 140pp; English.
XX CC The specification describes polypeptides that bind April or BAFF. The
    polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
    (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
    polypeptides of the invention are useful for treating immune-related
    diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
    lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
    sclerosis; or T-cell mediated disease such as graft rejection, graft
    versus host disease (GVHD) and inflammation. The present sequence
    represents a polypeptide of the invention, derived from formula II (see
    AEC02021), that that bind BAFF.
XX SQ Sequence 34 AA;
    Query Match 68.6%; Score 194; DB 9; Length 34;
    Best Local Similarity 97.1%; Pred. No. 9.7e-16;
    Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 43
AEC02025
ID AEC02025 standard; peptide; 34 AA.
XX AC AEC02025;
XX DT 20-OCT-2005 (first entry)
XX DE Formula II derived polypeptide D that binds BAFF.
XX KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX OS Synthetic.
XX PN WO2005075511-A1.
XX PD 18-AUG-2005.
XX PF 04-AUG-2004; 2004WO-US025247.
XX PR 29-JAN-2004; 2004US-0540271P.
XX PA (GETH ) GENENTECH INC.
XX PI Kelley RF, Patel D;
XX DR WPI; 2005-555932/56.
XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
    for treating immune-related disease, cancer or T-cell mediated disease
    such as graft rejection, graft versus host disease (GVHD) and
    inflammation.
XX PS Claim 7; SEQ ID NO 6; 140pp; English.
XX CC The specification describes polypeptides that bind APRIL or BAFF. The
    polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
    (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
    polypeptides of the invention are useful for treating immune-related
    diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
    lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
    sclerosis; or T-cell mediated disease such as graft rejection, graft
    versus host disease (GVHD) and inflammation. The present sequence
    represents a polypeptide of the invention that binds APRIL, derived from
    AEC02012.
XX SQ Sequence 34 AA;
    Query Match 68.6%; Score 194; DB 9; Length 34;
    Best Local Similarity 97.1%; Pred. No. 9.7e-16;
    Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 44
AEC02025
ID AEC02025 standard; peptide; 34 AA.
XX AC AEC02025;
XX DT 20-OCT-2005 (first entry)
XX DE Formula II derived polypeptide D that binds BAFF.
XX KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX OS Synthetic.
XX PN WO2005075511-A1.
XX PD 18-AUG-2005.
XX PF 04-AUG-2004; 2004WO-US025247.
XX PR 29-JAN-2004; 2004US-0540271P.
XX PA (GETH ) GENENTECH INC.
XX PI Kelley RF, Patel D;
XX DR WPI; 2005-555932/56.
XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
    for treating immune-related disease, cancer or T-cell mediated disease
    such as graft rejection, graft versus host disease (GVHD) and
    inflammation.
XX PS Claim 7; SEQ ID NO 6; 140pp; English.
XX CC The specification describes polypeptides that bind APRIL or BAFF. The
    polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
    (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
    polypeptides of the invention are useful for treating immune-related
    diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
    lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
    sclerosis; or T-cell mediated disease such as graft rejection, graft
    versus host disease (GVHD) and inflammation. The present sequence
    represents a polypeptide of the invention that binds APRIL, derived from
    AEC02012.
XX SQ Sequence 34 AA;
    Query Match 68.6%; Score 194; DB 9; Length 34;
    Best Local Similarity 97.1%; Pred. No. 9.7e-16;
    Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 45
AEC02017
ID AEC02017 standard; peptide; 34 AA.
XX AC AEC02017;
XX DT 20-OCT-2005 (first entry)
XX DE Formula I derived polypeptide F that binds APRIL.
XX KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX OS Synthetic.

```

```
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 13; SEQ ID NO 14; 140pp; English.
XX
XX The specification describes polypeptides that bind April or BAFF. The
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
XX polypeptides of the invention are useful for treating immune-related
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
XX sclerosis; or T-cell mediated disease such as graft rejection, graft
XX versus host disease (GVHD) and inflammation. The present sequence
XX represents a polypeptide of the invention, derived from formula II (see
XX AEC02021), that that bind BAFF.
XX
XX Sequence 34 AA;

Query Match      67.8%; Score 192; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.7e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
Db      1 CSQNEAFDSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 44
AEC02024
ID AEC02024 standard; peptide; 34 AA.
XX
XX AEC02024;
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula II derived polypeptide C that binds BAFF.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
XX
XX WO2005075511-A1.
XX
XX 18-AUG-2005.
XX
XX 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
XX
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
XX for treating immune-related disease, cancer or T-cell mediated disease
XX such as graft rejection, graft versus host disease (GVHD) and
XX inflammation.
XX
XX Claim 13; SEQ ID NO 13; 140pp; English.
XX
XX The specification describes polypeptides that bind April or BAFF. The
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
XX polypeptides of the invention are useful for treating immune-related
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
XX sclerosis; or T-cell mediated disease such as graft rejection, graft
XX versus host disease (GVHD) and inflammation. The present sequence
XX represents a polypeptide of the invention, derived from formula II (see
XX AEC02021), that that bind BAFF.
XX
XX Sequence 34 AA;

Query Match      67.8%; Score 192; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.7e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
Db      1 CSQNEAFDSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 45
AEC02020
ID AEC02020 standard; peptide; 34 AA.
XX
XX AEC02020;
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula I derived polypeptide I that binds APRIL.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
XX
XX WO2005075511-A1.
XX
XX 18-AUG-2005.
XX
XX 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
XX
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
XX for treating immune-related disease, cancer or T-cell mediated disease
XX such as graft rejection, graft versus host disease (GVHD) and
XX inflammation.
XX
XX Claim 7; SEQ ID NO 9; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
XX polypeptides of the invention are useful for treating immune-related
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
XX sclerosis; or T-cell mediated disease such as graft rejection, graft
XX versus host disease (GVHD) and inflammation. The present sequence
XX represents polypeptide of the invention that binds APRIL, derived from
XX AEC02012.
XX
XX Sequence 34 AA;

Query Match      67.5%; Score 191; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.2e-15;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
Db      1 CSQNEAFDSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 46
AEC02018
```



ID AEC02018 standard; peptide; 34 AA.  
 XX  
 AC AEC02018;  
 XX  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 DE Formula I derived polypeptide G that binds APRIL.  
 XX  
 XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005075511-A1.  
 PN  
 XX  
 XX 18-AUG-2005.  
 PD  
 XX  
 XX 04-AUG-2004; 2004WO-US025247.  
 PF  
 XX  
 XX 29-JAN-2004; 2004US-0540271P.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Kelley RF, Patel D;  
 PI  
 XX  
 XX WPI; 2005-555932/56.  
 DR  
 XX  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX  
 XX Claim 7; SEQ ID NO 7; 140pp; English.  
 PS  
 XX  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC scleroma; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents polypeptide of the invention that binds APRIL, derived from  
 CC AEC02012.  
 XX  
 XX Sequence 34 AA;  
 SQ  
 Query Match 66.8%; Score 189; DB 9; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 3.8e-15;  
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX  
 QY 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41  
 |||||  
 Db 1 CSQNEYFDSLHACIPCDLRCSSNTPLTCQRYC 34  
 |||||  
 RESULT 47  
 AEC02029  
 ID AEC02029 standard; peptide; 34 AA.  
 XX  
 XX  
 AC AEC02029;  
 XX  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 XX Formula II derived polypeptide H that binds BAFF.  
 DE  
 XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005075511-A1.  
 PN  
 XX  
 XX 18-AUG-2005.  
 PD  
 XX  
 XX 04-AUG-2004; 2004WO-US025247.  
 PF  
 XX  
 XX 29-JAN-2004; 2004US-0540271P.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Kelley RF, Patel D;  
 PI  
 XX  
 XX WPI; 2005-555932/56.  
 DR  
 XX  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX  
 XX Claim 7; SEQ ID NO 7; 140pp; English.  
 PS  
 XX  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC scleroma; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents polypeptide of the invention that binds APRIL, derived from  
 CC AEC02012.  
 XX  
 XX Sequence 34 AA;  
 SQ  
 Query Match 66.8%; Score 189; DB 9; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 3.8e-15;  
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX  
 QY 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41  
 |||||  
 Db 1 CSQNEYFDSLHACIPCDLRCSSNTPLTCQRYC 34  
 |||||  
 RESULT 47  
 AEC02029  
 ID AEC02029 standard; peptide; 34 AA.  
 XX  
 XX  
 AC AEC02029;  
 XX  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 XX Formula II derived polypeptide H that binds BAFF.  
 DE  
 XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005075511-A1.  
 PN  
 XX  
 XX 18-AUG-2005.  
 PD  
 XX  
 XX 04-AUG-2004; 2004WO-US025247.  
 PF  
 XX  
 XX 29-JAN-2004; 2004US-0540271P.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Kelley RF, Patel D;  
 PI  
 XX  
 XX WPI; 2005-555932/56.  
 DR  
 XX  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX  
 XX Claim 7; SEQ ID NO 7; 140pp; English.  
 PS  
 XX  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC scleroma; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents polypeptide of the invention that binds APRIL, derived from  
 CC AEC02012.  
 XX  
 XX Sequence 34 AA;  
 SQ

PD 18-AUG-2005.  
 XX  
 XX 04-AUG-2004; 2004WO-US025247.  
 PF  
 XX  
 XX 29-JAN-2004; 2004US-0540271P.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Kelley RF, Patel D;  
 PI  
 XX  
 XX WPI; 2005-555932/56.  
 DR  
 XX  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX  
 XX Claim 13; SEQ ID NO 18; 140pp; English.  
 PS  
 XX  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC scleroma; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents a polypeptide of the invention, derived from formula II (see  
 CC AEC02021), that that bind BAFF.  
 XX  
 XX Sequence 34 AA;  
 SQ  
 Query Match 66.8%; Score 189; DB 9; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 3.8e-15;  
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX  
 QY 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41  
 |||||  
 Db 1 CSQNEYFDSLHACIPCDLRCSSNTPLTCQRYC 34  
 |||||  
 RESULT 48  
 AEC02019  
 ID AEC02019 standard; peptide; 34 AA.  
 XX  
 XX  
 AC AEC02019;  
 XX  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 XX Formula I derived polypeptide H that binds APRIL.  
 DE  
 XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005075511-A1.  
 PN  
 XX  
 XX 18-AUG-2005.  
 PD  
 XX  
 XX 04-AUG-2004; 2004WO-US025247.  
 PF  
 XX  
 XX 29-JAN-2004; 2004US-0540271P.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Kelley RF, Patel D;  
 PI  
 XX  
 XX WPI; 2005-555932/56.  
 DR  
 XX  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX  
 XX Claim 13; SEQ ID NO 18; 140pp; English.  
 PS  
 XX  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC scleroma; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents a polypeptide of the invention, derived from formula II (see  
 CC AEC02021), that that bind BAFF.  
 XX  
 XX Sequence 34 AA;  
 SQ

PT inflammation.

XX

PS Claim 7; SEQ ID NO 8; 140pp; English.

XX

CC The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis factor (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerosis; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents polypeptide of the invention that binds APRIL, derived from AEC02012.

XX

CC

SQ Sequence 34 AA;

Query Match 64.3%; Score 182; DB 9; Length 34;

Best Local Similarity 91.2%; Pred. No. 2.6e-14;

Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPELTQRYC 41

DB 1 CSQNEYFDSLHACKPCDLYCSNTPELTQRYC 34

RESULT 49

AAB08844

ID AAB08844 standard; peptide; 185 AA.

XX

AC AAB08844;

XX

DT 02-JAN-2001 (first entry)

XX

DE Amino acid sequence of murine BCMA polypeptide.

XX

KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;

KW anti-cell death gene; apoptosis; viral infection; inflammatory response;

KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX

OS Mus musculus.

XX

PH Key Location/Qualifiers

FT Domain 47..72

FT /note= "putative transmembrane domain"

XX

XX WO200005633-A1.

XX

XX 31-AUG-2000.

XX

XX 24-FEB-2000; 2000WO-US004925.

XX

XX 24-FEB-1999; 99US-0121485P.

XX

XX (GEO ) GEN HOSPITAL CORP.

XX

XX Seed B, Ting A;

XX

XX WPI; 2000-558405/51.

XX

XX Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene expression.

XX

XX Claim 32; Fig 7B; 53pp; English.

XX

CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a

CC recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug designing

CC

SQ Sequence 185 AA;

Query Match 64.0%; Score 181; DB 3; Length 185;

Best Local Similarity 70.8%; Pred. No. 2e-13;

Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGQSQNEYFDSLHACIPQLRCSSNTPELTQRYCNASVTNSVKG 51

DB 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46

RESULT 50

AAAY71980

ID AAY71980 standard; protein; 185 AA.

XX

AC AAY71980;

XX

DT 28-MAR-2001 (first entry)

XX

DE Murine B cell maturation factor (BCMA) protein.

XX

KW Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;

KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;

KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;

KW haenolytic anemia; Grave's disease; myasthenia gravis; BCMA;

KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;

KW post-streptococcal glomerulonephritis; polyarteritis nodosa.

XX

OS Mus musculus.

XX

XX WO2000068378-A1.

XX

XX 16-NOV-2000.

XX

XX 05-MAY-2000; 2000WO-US012266.

XX

XX 06-MAY-1999; 99US-0132892P.

PR 01-MAY-2000; 2000US-0201012P.

XX

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX

XX Shu HS;

XX

XX WPI; 2001-016094/02.

XX

XX N-PSDB; AAD02130.

XX

XX Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.

PT

PT

XX

PS Claim 37; Page 107-108; 112pp; English.

XX

CC The present invention relates to Tumour necrosis factor (TNF) and Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte

CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus  
CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple  
CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,  
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal  
CC Glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its  
CC corresponding nucleic acid sequence are also useful in diagnostic assays.  
CC The present sequence is a murine B cell maturation factor (BCMA). BCMA is  
CC the receptor for TALL-1 protein  
XX  
SQ Sequence 185 AA;  
  
Query Match 64.0%; Score 181; DB 4; Length 185;  
Best Local Similarity 70.8%; Pred. No. 2e-13;  
Matches 34; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
  
QY 4 MAQCQSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 MAQCQFHSYFDSLHACKPCHLRCNS--PPATCQPCDPSVTSSVKG 46  
  
RESULT 51  
AAE15490  
ID AAE15490 standard; protein; 185 AA.  
XX AAE15490;  
AC  
DT 12-MAR-2002 (first entry)  
XX  
DE Mouse B cell maturation (BCMA) protein.  
XX  
KW Mouse; transmembrane activator and intracellular CAML interactor; TACI;  
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX  
OS Mus sp.  
XX  
XX W0200187979-A2.  
PN  
XX 22-NOV-2001.  
PD  
XX  
XX 14-MAY-2001; 2001WO-US015567.  
PF  
XX  
XX 12-MAY-2000; 2000US-0204039P.  
PR  
XX 27-JUN-2000; 2000US-0214591P.  
PR  
XX 14-MAY-2001; 2001US-00214591.  
PR  
XX  
PA (AMGE-) AMGEN INC.  
XX  
XX Theill LE, Yu G;  
PI  
XX WPI; 2002-066686/09.  
DR  
XX  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
XX activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
PT  
XX  
PS Disclosure; Fig 11; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell

CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is mouse BCMA protein  
XX  
SQ Sequence 185 AA;  
  
Query Match 64.0%; Score 181; DB 5; Length 185;  
Best Local Similarity 70.8%; Pred. No. 2e-13;  
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;  
  
QY 4 MAQCQSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 MAQCQFHSYFDSLHACKPCHLRCNS--PPATCQPCDPSVTSSVKG 46  
  
RESULT 52  
ADZ67762  
ID ADZ67762 standard; protein; 185 AA.  
XX ADZ67762;  
AC  
DT 14-JUL-2005 (first entry)  
XX  
DE Mouse tumor necrosis factor receptor BCMA.  
XX  
KW Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;  
KW cytostatic.  
XX  
OS Mus musculus.  
XX W020005037865-A2.  
PN  
XX 28-APR-2005.  
PD  
XX  
XX 18-OCT-2004; 2004WO-US034375.  
PF  
XX  
XX 16-OCT-2003; 2003US-0511698P.  
PR  
XX 18-OCT-2004; 2004US-0619552P.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX  
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;  
PI  
XX WPI; 2005-315682/32.  
DR  
XX  
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
XX detecting ligands, and for modulating tumor growth, metastasis and  
XX immunity, such as separating resting from stimulated immune cells.  
XX  
XX Disclosure; SEQ ID NO 10; 132pp; English.  
XX  
PS The invention provides novel tumor necrosis factor receptor ztnfr14  
XX polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors  
XX and antibodies. Human ztnfr14 polynucleotides are used in claimed methods  
XX for detecting a genetic abnormality in a patient and for detecting a  
XX cancer in a patient. Recombinant ztnfr14 polypeptide, optionally  
XX conjugated to a toxin, is used in a claimed method of killing cancer  
XX cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and  
XX antagonists. The polypeptides, polynucleotides and antibodies may also be  
XX used in methods that modulate tumor growth, metastasis, and immunity such  
XX as separating resting from stimulated immune cells. The present sequence  
XX is that of murine TNFR BCMA. This sequence was compared with that of  
XX murine ztnfr14 ADZ67756 in the identification of ztnfr14 as a member of  
XX the TNFR family.

SQ	Sequence 185 AA;	CC	sclerosis, rheumatoid arthritis, systemic lupus erythematosus, fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is mouse BCMA protein-human immunoglobulin Fc region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
QY	4 MAGQCSQNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTNSVKG 51	CC	
DB	1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46	CC	
AAE15489	AAE15489 standard; protein; 281 AA.	CC	
AAE15489;		CC	
29-AUG-2003 (revised)		CC	
12-MAR-2002 (first entry)		CC	
Mouse BCMA-human immunoglobulin Fc region fusion protein.		CC	
Human; transmembrane activator and intracellular CAML interactor; TACI; cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein; mouse.		CC	
Homo sapiens.		CC	
Mus sp.		CC	
Chimeric.		CC	
WO200187979-A2.		CC	
22-NOV-2001.		CC	
14-MAY-2001; 2001WO-US015567.		CC	
12-MAY-2000; 2000US-0204039P.		CC	
27-JUN-2000; 2000US-0214591P.		CC	
14-MAY-2001; 2001US-00214591.		CC	
(AMGE-) AMGEN INC.		CC	
Theill LE, Yu G;		CC	
WPI; 2002-066686/09.		CC	
Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand.		CC	
Disclosure; Fig 10B; 94pp; English.		CC	
The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple		CC	
Query Match 64.0%; Score 181; DB 9; Length 185;		CC	
Best Local Similarity 70.8%; Pred. No. 2e-13;		CC	
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;		CC	
QY	4 MAGQCSQNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTNSVKG 51	CC	
DB	1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46	CC	
AAE15489	AAE15489 standard; protein; 281 AA.	CC	
AAE15489;		CC	
29-AUG-2003 (revised)		CC	
12-MAR-2002 (first entry)		CC	
Mouse BCMA-human immunoglobulin Fc region fusion protein.		CC	
Human; transmembrane activator and intracellular CAML interactor; TACI; cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein; mouse.		CC	
Homo sapiens.		CC	
Mus sp.		CC	
Chimeric.		CC	
WO200187979-A2.		CC	
22-NOV-2001.		CC	
14-MAY-2001; 2001WO-US015567.		CC	
12-MAY-2000; 2000US-0204039P.		CC	
27-JUN-2000; 2000US-0214591P.		CC	
14-MAY-2001; 2001US-00214591.		CC	
(AMGE-) AMGEN INC.		CC	
Theill LE, Yu G;		CC	
WPI; 2002-066686/09.		CC	
Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand.		CC	
Disclosure; Fig 10B; 94pp; English.		CC	
The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple		CC	
Query Match 64.0%; Score 181; DB 5; Length 281;		CC	
Best Local Similarity 70.8%; Pred. No. 3.2e-13;		CC	
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;		CC	
QY	4 MAGQCSQNEYFDSLHACIPCOLRCSNTPTLTQRYCNASVTNSVKG 51	CC	
DB	1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46	CC	
RESULT 54		CC	
ABJ38417		CC	
ID	ABJ38417 standard; protein; 42 AA.	CC	
XX	ABJ38417;	CC	
AC	ABJ38417;	CC	
XX		CC	
DT	12-JUN-2003 (first entry)	CC	
XX		CC	
DE	TALL-1 related protein SEQ ID No 197.	CC	
XX		CC	
KW	TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease; systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis; Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis; gene therapy.	CC	
OS	Homo sapiens.	CC	
OS	WO200292620-A2.	CC	
PN		CC	
XX		CC	
PD	21-NOV-2002.	CC	
XX		CC	
PF	13-MAY-2002; 2002WO-US015273.	CC	
PR		CC	
PR	11-MAY-2001; 2001US-0290196P.	CC	
XX		CC	
PA	(AMGE-) AMGEN INC.	CC	
XX		CC	
PI	Min H, Hsu H;	CC	
XX		CC	
DR	WPI; 2003-156719/15.	CC	
XX		CC	
PT	New TALL-1-binding polypeptide, useful for modulating the activity of TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.	CC	
PT		CC	
XX		CC	
PS	Disclosure; Page 26; 236pp; English.	CC	
XX		CC	
CC	The invention relates to a novel TALL-1-binding polypeptide comprising a defined sequence in the specification. The composition is useful in ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, asthma, atherosclerosis, cachexia, cirrhosis, diabetes, glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis and vasculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a TALL-1 related protein of the invention	CC	
XX	Sequence 42 AA;	CC	

```
Query Match      55.8%; Score 158; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLQWAGCQSQNEYFDSLHACIPQLRC 28
Db      15 MLQWAGCQSQNEYFDSLHACIPQLRC 42
        |||||
RESULT 55
ADI53060
ID      ADI53060 standard; peptide; 26 AA.
XX
AC      ADI53060;
XX
DT      22-APR-2004 (first entry)
XX
DE      Human BCMA receptor binding site.
XX
KW      protein co-ordinate data; cytostatic; anti-allergic; immunosuppressive;
KW      antirheumatic; antiarthritic; neuroprotective; anti-inflammatory;
KW      antidiabetic; dermatological; antiasthmatic; neutrokin-alpha;
KW      crystallography; cancer; allergic disorder; autoimmune disease;
KW      rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
KW      systemic lupus erythematosus; asthma; receptor.
XX
OS      Homo sapiens.
XX
PN      WO2003050134-A2.
XX
PD      19-JUN-2003.
XX
PF      07-NOV-2002; 2002WO-US035661.
XX
PR      07-NOV-2001; 2001US-0331049P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Li Y, Oren DE, Arnold E, Volovik Y;
XX
WPI; 2003-532895/50.
XX
PT      New crystalline Neutrokin-alpha protein, useful for designing compounds
PT      that bind, inhibit or mimic a Neutrokin-alpha protein or enhance the
PT      activity of a Neutrokin-alpha protein for treating e.g. cancer or
PT      allergic disorders.
XX
PS      Disclosure; Fig 4; 362pp; English.
XX
CC      The invention relates to a neutrokin-alpha protein in crystalline form.
CC      The crystalline neutrokin-alpha protein is useful for designing
CC      molecules that have biological activity or compounds that bind, inhibit
CC      or mimic a neutrokin-alpha protein and/or enhance the activity of a
CC      neutrokin-alpha protein. The three-dimensional structure of a neutrokin-
CC      alpha protein is useful in determining the three-dimensional of other
CC      neutrokin-alpha proteins and their homologs. The compounds that mimic,
CC      prevent or inhibit the activity of the protein are useful for treating
CC      cancer, allergic disorders, or autoimmune diseases such as rheumatoid
CC      arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
CC      erythematosus or asthma. This sequence represents the residues in the
CC      receptor for binding a cytokine ligand.
XX
SQ      Sequence 26 AA;

Query Match      53.4%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EYFDSLHACIPQLRCSSNTPPLTC 37
Db      1 EYFDSLHACIPQLRCSSNTPPLTC 26
        |||||
us-10-077-137-1_copy_1_51.rag
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RESULT 56
AAE15491
ID      AAE15491 standard; protein; 117 AA.
XX
AC      AAE15491;
XX
DT      29-AUG-2003 (revised)
DT      12-MAR-2002 (first entry)
XX
DE      Human-murine B cell maturation protein (BCMA) consensus sequence.
XX
KW      Human; transmembrane activator and intracellular CAML interactor; TACI;
KW      cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW      lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW      prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW      drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW      Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW      human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW      rheumatoid arthritis; atherosclerosis; mouse.
XX
OS      Homo sapiens.
XX
OS      Mus sp.
XX      Chimeric.
XX
PN      WO200187979-A2.
XX
PD      22-NOV-2001.
XX
PF      14-MAY-2001; 2001WO-US015567.
XX
PR      12-MAY-2000; 2000US-0204039P.
PR      27-JUN-2000; 2000US-0214591P.
PR      14-MAY-2001; 2001US-00214591.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Theill LE, Yu G;
XX
WPI; 2002-066686/09.
XX
PT      Inhibiting activity of B cell maturation protein and/or transmembrane
PT      activator and intracellular cyclophilin ligand interactor, by
PT      administering a binding partner for APRIL, a tumor necrosis factor family
PT      ligand.
XX
PS      Disclosure; Fig 11; 94pp; English.
XX
CC      The invention relates to a method for inhibiting TACI (transmembrane
CC      activator and intracellular CAML interactor) and/or B cell maturation
CC      protein (BCMA) activity in a mammal. The method comprises administering a
CC      specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC      family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC      BCMA extracellular consensus sequence, but not the extracellular region
CC      of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC      and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC      lymphoproliferative disorders, one or more solid tumours such as lung,
CC      gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC      antagonists are useful for treating inflammation and immune function
CC      diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC      dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC      disease), drug and insect sting allergy, inflammatory bowel disease
CC      (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC      sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC      bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC      with leucocyte infiltration of the skin or organs. The present sequence
CC      is human-murine B cell maturation protein (BCMA) consensus sequence.
CC      (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ      Sequence 117 AA;

Query Match      36.7%; Score 104; DB 5; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.00019;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;
```



Qy 8 CSONEYFSLHHACIPQLRCSNTPPLTCQRYC 41

Dd 6 CPKDOYWDSSRKSCVSCALITCSORS-QRTCTDFC 38

XX  
DE  
number nocuous factor receptor superfamily member 13b protein. SEO: 54.

KW Plasma membrane; diagnosis; therapeutic; cancer; cytostatic; neoplasm;  
KW tumor necrosis factor receptor.  
XX  
OS Mus musculus.  
XX  
PN WO2005052182-A2.  
XX  
XX  
PD 09-JUN-2005.  
XX  
PF 25-NOV-2004; 2004WO-IL001085.  
XX  
PR 26-NOV-2003; 2003US-0524885P.  
XX  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
XX  
XX Linial M, Inberg A, Bledi Y;  
XX WPI; 2005-418017/42.  
DR REFSEQ; NP\_067324.  
XX  
XX Characterizing proteins present in a plasma membrane of a cell, useful in  
PT identifying diagnostic markers and potential drugs, comprises subjecting  
PT a cell to a protease treatment.  
XX  
XX Claim 25; SEQ ID NO 54; 196pp; English.  
PS  
XX  
CC The present invention relates to a method of characterizing proteins  
CC present in the plasma membrane (PM) of live cells. The proteins of the  
CC invention are useful in identifying diagnostic markers and potential  
CC drugs. The invention is useful for identifying drugs for diagnosing and  
CC treating disorders such as cancer which are associated with abnormal  
CC representation of cell surface proteins. The present sequence is mouse  
CC tumor necrosis factor receptor superfamily member 13b protein.  
XX  
SQ Sequence 249 AA;

Query Match 25.3%; Score 71.5; DB 9; Length 249;  
Best Local Similarity 35.3%; Pred. No. 3.1;  
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;  
QY 8 CSQNEYFDSLHLHACIPCOLRCSSNTPLTQRYC 41  
DB 6 CPKQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38

RESULT 62  
ADC71568  
ID ADC71568 standard; protein; 1548 AA.  
AC ADC71568;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Mouse subtilisin-like protein convertase 6 (SPC6).  
XX  
KW neuroleptic; subtilisin-like protein convertase 6 agonist;  
KW subtilisin-like protein convertase 6 antagonist; transgenic;  
KW subtilisin-like protein convertase 6; SPC6; schizophrenia.  
XX  
OS Mus sp.  
XX  
PN US2003093824-A1.  
XX  
XX 15-MAY-2003.  
XX  
XX 25-JUN-2002; 2002US-00180903.  
XX  
XX 26-JUN-2001; 2001US-0300978P.  
PR 24-SEP-2001; 2001US-0324820P.  
XX  
XX (ALLE/) ALLEN K D.  
XX Allen KD;  
XX  
PT New subtilase-encoding polynucleotide and its encoded protein, useful for

XX  
DR WPI; 2003-777261/73.  
DR N-PSDB; ADC71567.  
XX  
XX New transgenic mouse useful in methods for identifying potential  
PT therapeutic agents for treating a variety of diseases, including  
PT schizophrenia, comprises a disruption in a subtilisin-like protein  
PT convertase 6 (SPC6) gene.  
XX  
XX Disclosure; SEQ ID NO 2; 34pp; English.  
XX  
XX The invention describes a transgenic mouse (I) comprising a disruption in  
CC an subtilisin-like protein convertase (SPC6) gene, where there is no  
CC native expression of an endogenous SPC6 gene. The therapeutic agent is  
CC administered by inhalation or insufflation or oral, buccal, parenteral,  
CC topical, subcutaneous, intraperitoneal, intravenous, intrapleural,  
CC intraocular, intraarterial, or rectal route. The transgenic mouse and  
CC associated methods are useful for identifying potential therapeutic  
CC agents (e.g. SPC6 agonists and antagonists) for treating conditions  
CC associated with SPC6. The identified agents are potentially useful for  
CC treating diseases such as schizophrenia. The mouse is useful for  
CC investigating the biological roles of SPC6. This is the amino acid  
CC sequence of mouse SPC6.  
XX  
SQ Sequence 1548 AA;

Query Match 24.9%; Score 70.5; DB 7; Length 1548;  
Best Local Similarity 34.7%; Pred. No. 28;  
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

QY 7 QCSQNEYFDSLHLHACIPCOLRCSSNTPP-----LTCQRYCNASVTNSVK 50  
DB 1151 ECAAVEYWDSESHRCQPCHKKCRCSGSEDCQYTCPRETFLNTTCVK 1199

RESULT 63  
ABB80243  
ID ABB80243 standard; protein; 1877 AA.  
XX  
AC ABB80243;

XX 04-DEC-2003 (first entry)  
XX  
XX Murine subtilase.

XX Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney;  
KW renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;  
KW pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;  
KW proprotein convertase subtilisin; furin-like repeat; Alzheimer's disease;  
KW Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;  
KW gastritis; ulcers; urinary incontinence; lupus nephritis;  
KW renal transplant rejection; myocardial infarction; erectile dysfunction;  
KW ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;  
KW congestive heart failure; ischaemia; hypertensive vascular disease.  
XX  
OS Mus musculus.  
XX  
XX WO2003060109-A2.  
PN  
XX  
XX 24-JUL-2003.  
XX  
XX 14-JAN-2003; 2003WO-EP000253.  
XX  
XX 15-JAN-2002; 2002US-0347876P.  
PR 29-JUL-2002; 2002US-0398734P.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Koehler RH;  
PI  
XX WPI; 2003-608065/57.  
XX  
XX New subtilase-encoding polynucleotide and its encoded protein, useful for





DR GENBANK; AAQ82434.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,

PT e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

XX Example 2; Fig 1; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The mucin-like proteins and coding sequences are useful

CC in the therapy or in the prevention of a disease when the increase in the

CC mucin-like activity of a polypeptide is needed e.g. bacterial infections,

CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

CC wounding, inflammatory bowel disease, Crohn's disease, small

CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

CC chronic cholecystitis, or skin cancer. The present sequence is a mucin

CC glycoprotein which was used in a sequence alignment with the mucin-like

CC proteins of the invention.

XX

SQ Sequence 1569 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 1569;

Best Local Similarity 45.2%; Pred. No. 50;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQ 38

||||| :|||

Db 1179 CSQDEYFDHEGVCFPCM-----PPTPQ 1202

RESULT 66

ADR18914

ID ADR18914 standard; protein; 2240 AA.

XX

AC ADR18914;

XX

DT 04-NOV-2004 (first entry)

XX

DE Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.

XX

KW Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;

KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT Peptide 1..18

FT Protein /label= Signal\_peptide

FT /label= Mature\_protein

XX

PN WO2004069136-A2.

XX

PD 19-AUG-2004.

XX

PF WO2004069136-A2.

XX

PD 19-AUG-2004.

XX

PF 04-FEB-2004; 2004WO-EP050082.

XX

PR 05-FEB-2003; 2003US-0445217P.

XX

PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX

PI Bienkowska J, Mcallister G;

XX

DR WPI; 2004-604324/58.

XX

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,

PT e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

XX

PS Claim 2; SEQ ID NO 4; 170pp; English.

CC The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The present sequence is one such human mucin-like

CC protein. The mucin-like proteins and coding sequences are useful in the

CC therapy or in the prevention of a disease when the increase in the mucin-

CC like activity of a polypeptide is needed e.g. bacterial infections,

CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

CC wounding, inflammatory bowel disease, Crohn's disease, small

CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

CC chronic cholecystitis, or skin cancer.

XX

SQ Sequence 2240 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2240;

Best Local Similarity 45.2%; Pred. No. 73;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQ 38

||||| :|||

Db 1161 CSQDEYFDHEGVCFPCM-----PPTPQ 1184

RESULT 67

ADR18913

ID ADR18913 standard; protein; 2258 AA.

XX

AC ADR18913;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human mucin-like protein, SCS0004, variant SEQ ID 3.

XX

KW Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;

KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT Peptide 1..18

FT Protein /label= Signal\_peptide

FT /label= Mature\_protein

XX

PN WO2004069136-A2.

XX

PD 19-AUG-2004.

XX

PF 04-FEB-2004; 2004WO-EP050082.

XX

PR 05-FEB-2003; 2003US-0445217P.

XX

PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX

PI Bienkowska J, Mcallister G;

XX

DR WPI; 2004-604324/58.

XX

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,

PT e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

XX

PS Claim 2; SEQ ID NO 3; 170pp; English.

XX

CC The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The present sequence is one such human mucin-like

CC protein. The mucin-like proteins and coding sequences are useful in the

CC therapy or in the prevention of a disease when the increase in the mucin-

CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.

XX Sequence 2258 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2258;

Best Local Similarity 45.2%; Pred. No. 73;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQ 38

DB 1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202

RESULT 68

ADRL8915

ID ADRL8915 standard; protein; 2264 AA.

XX AC ADRL8915;

XX DT 04-NOV-2004 (first entry)

XX DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.

XX KW Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

XX KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;

XX KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

XX KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

XX KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

XX KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

XX KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX OS Homo sapiens.

XX PN WO2004069136-A2.

XX PD 19-AUG-2004.

XX PF 04-FEB-2004; 2004WO-EP050082.

XX PR 05-FEB-2003; 2003US-0445217P.

XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX PI Bienkowska J, Mcallister G;

XX PS WPI; 2004-604324/58.

XX DR New isolated mucin-like polypeptides, useful for diagnosing or treating,

XX PT e.g. bacterial infections, allergic asthma, inflammation, allergic

XX PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

XX PT cancer, or skin cancer.

XX PS Claim 2; SEQ ID NO 5; 170pp; English.

XX CC The present invention relates to novel mucin-like proteins (I) and their

XX CC coding sequences. The present sequence is one such human mucin-like

XX CC protein. The mucin-like proteins and coding sequences are useful in the

XX CC therapy or in the prevention of a disease when the increase in the mucin-

XX CC like activity of a polypeptide is needed e.g. bacterial infections,

XX CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

XX CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

XX CC wounding, inflammatory bowel disease, Crohn's disease, small

XX CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

XX CC chronic cholecystitis, or skin cancer.

XX SQ Sequence 2264 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2264;

Best Local Similarity 45.2%; Pred. No. 73;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQ 38

DB 1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202

RESULT 69

AAU10951

ID AAU10951 standard; protein; 37 AA.

XX AC AAU10951;

XX DT 12-MAR-2002 (first entry)

XX DE Human AGP-3 receptor cysteine rich repeat region #1.

XX KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;

XX KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;

XX KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;

XX KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;

XX KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;

XX KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;

XX KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;

XX KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;

XX KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;

XX KW multiple sclerosis; Parkinson's disease; transgenic animal.

XX OS Homo sapiens.

XX PN WO200185782-A2.

XX PD 15-NOV-2001.

XX PF 12-FEB-2001; 2001WO-US004568.

XX PR 11-FEB-2000; 2000US-0181800P.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Hsu H;

XX WPI; 2002-049441/06.

XX CC Composition, useful for identifying modulator of receptor for treating

XX PT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor

XX PT ligand family member) receptor and encoding nucleic acids.

XX PS Claim 1; Fig 18; 124pp; English.

XX CC The invention relates to a composition (I) comprising AGP-3 receptor

XX CC (tumour necrosis factor ligand family member) related protein (II)

XX CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related

XX CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in

XX CC assays to identify cells and tissues that express AGP-3R or proteins

XX CC related to AGP-3R-related protein and for identifying compounds (agonists

XX CC or antagonists) that interact with AGP-3R proteins. (II) is also useful

XX CC for identifying intracellular proteins that interact with the respective

XX CC cytoplasmic domains by yeast two-hybrid screening processes. (II) is

XX CC involved in B cell growth, survival and activation particularly in lymph

XX CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists

XX CC identified using (II) are used for modulating B cell response and are

XX CC used to treat diseases characterised by inflammatory processes or

XX CC deregulated immune response such as rheumatoid arthritis, graft-versus-

XX CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the

XX CC production of hybridoma cells which are derived from B cells, which

XX CC involves treating the hybridoma cells with (II). (II) is useful in the

XX CC treatment of inflammatory conditions of joints, e.g., rheumatoid

XX CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are

XX CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis

XX CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,

XX CC diabetes, fever, glomerulonephritis, inflammatory bowel disease,



Query Match		23.9%;	Score 67.5;	DB 5;	Length 59;
Best Local Similarity		30.6%;	Pred. No. 2.1;	Mismatches 11;	Conservative 9;
Matches		11;	Gaps	1;	Indels 15;
QY	8 CSQNEFYDLSLLHACIPQCLRCSSNTPLTCQRYCNA	43			
DB	1 CPEEQWDPDLGTCMSCKTICNHQS-QRTCAAFCS	35			
RESULT 72					
AAW75785					
ID	AAW75785	standard; protein; 166 AA.			
XX	XX				
AC	AAW75785;				
XX	XX				
DT	18-JAN-1999	(first entry)			
DE	Human lymphocyte surface receptor extracellular domain.				
XX	XX				
KW	TACI; transmembrane activator and CAML-interactor;				
KW	calcium signal-modulating cyclophilin ligand; human;				
KW	lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;				
KW	cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;				
KW	immunosuppressive; graft versus host disease; transplant rejection;				
KW	therapy; signal transduction.				
XX	XX				
OS	Homo sapiens.				
XX	XX				
PN	W09839361-A1.				
XX	XX				
PD	11-SEP-1998.				
XX	XX				
PF	03-MAR-1998;	98WO-US004270.			
XX	XX				
PR	03-MAR-1997;	97US-00810572.			
XX	XX				
PA	(STUD-) ST JUDE CHILDREN'S RES HOSPITAL.				
XX	XX				
PI	Bram RJ, Von Bulow G;				
XX	XX				
DR	WPI; 1998-506346/43.				
DR	N-PSDB; AAV57330.				
XX	XX				
PT	New isolated transmembrane activator protein - used to develop products				
PT	for treating e.g. infections, cancers, autoimmune and inflammatory				
PT	conditions, transplant rejection or graft-versus-host disease.				
XX	XX				
PS	Claim 8; Page 73; 89pp; English.				
XX	XX				
CC	This is the amino acid sequence of the N-terminal, i.e. the				
CC	extracellular, domain of novel human transmembrane activator and CAML-				
CC	interactor (TACI) protein (see AAW75783). TACI is a lymphocyte receptor				
CC	protein that is involved in the calcium activation pathway. It is				
CC	normally present in B-lymphocytes, and to a much lesser extent in				
CC	immature T-lymphocytes, and can therefore be targeted to specifically				
CC	regulate B cell responses without affecting T cell activity. The				
CC	extracellular domain of TACI functions as a binding site for a ligand				
CC	that stimulates the activation of the cell by inducing the binding of the				
CC	C-terminal portion (see AAW75784) of TACI to the N-terminal domain of				
CC	CAML. A recombinant form of the extracellular portion of TACI acts as a				
CC	dominant-negative or blocking agent and acts to suppress the immune				
CC	system. It can be used to treat or prevent autoimmune disease, graft				
CC	rejection or graft versus host disease. The extracellular region is also				
CC	used in a claimed method for identifying a ligand for TACI, in which				
CC	binding of a candidate molecule is determined by detecting cellular				
CC	activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription				
CC	factor, or of NF-AT dependent transcription				
XX	XX				
SQ	Sequence 166 AA;				
Query Match					
Best Local Similarity		23.9%;	Score 67.5;	DB 2;	Length 166;
Matches		11;	Gaps	1;	Indels 15;
Query Match					
Best Local Similarity		23.9%;	Score 67.5;	DB 5;	Length 166;
Matches		11;	Gaps	1;	Indels 15;

QY	8 CSQNEFYDLSLLHACIPQCLRCSSNTPLTCQRYCNA	43			
DB	34 CPEEQWDPDLGTCMSCKTICNHQS-QRTCAAFCS	68			
RESULT 73					
AAE15494					
ID	AAE15494	standard; protein; 166 AA.			
XX	XX				
AC	AAE15494;				
XX	XX				
DT	12-MAR-2002	(first entry)			
XX	XX				
DE	Human TACI extracellular domain.				
XX	XX				
KW	Human; transmembrane activator and intracellular CAML interactor; TACI;				
KW	cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;				
KW	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;				
KW	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;				
KW	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;				
KW	Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;				
KW	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;				
KW	rheumatoid arthritis; atherosclerosis.				
XX	XX				
OS	Homo sapiens.				
XX	XX				
PN	W0200187979-A2.				
XX	XX				
PD	22-NOV-2001.				
XX	XX				
PF	14-MAY-2001;	2001WO-US015567.			
XX	XX				
PR	12-MAY-2000;	2000US-0204039P.			
XX	XX				
PR	27-JUN-2000;	2000US-0214591P.			
XX	XX				
PR	14-MAY-2001;	2001US-00214591.			
XX	XX				
PA	(AMGE-) AMGEN INC.				
XX	XX				
PI	Theill LE, Yu G;				
XX	XX				
DR	WPI; 2002-066686/09.				
XX	XX				
PT	Inhibiting activity of B cell maturation protein and/or transmembrane				
PT	activator and intracellular cyclophilin ligand interactor, by				
PT	administering a binding partner for APRIL, a tumor necrosis factor family				
PT	ligand.				
XX	XX				
PS	Claim 1; Fig 12A; 94pp; English.				
XX	XX				
CC	The invention relates to a method for inhibiting TACI (transmembrane				
CC	activator and intracellular CAML interactor) and/or B cell maturation				
CC	protein (BCMA) activity in a mammal. The method comprises administering a				
CC	specific binding partner for APRIL (G70, a tumour necrosis factor-TNF				
CC	family ligand), having the consensus region of TACI, BCMA, or the TACI/				
CC	BCMA extracellular consensus sequence, but not the extracellular region				
CC	of TACI or BCMA. The method is useful for inhibiting activity of TACI				
CC	and/or BCMA in a mammal which is useful for treating B-cell or T-cell				
CC	lymphoproliferative disorders, one or more solid tumours such as lung,				
CC	gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI				
CC	antagonists are useful for treating inflammation and immune function				
CC	diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic				
CC	dermatitis, respiratory allergic disease (asthma, hypersensitivity lung				
CC	disease), drug and insect sting allergy, inflammatory bowel disease				
CC	(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple				
CC	sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,				
CC	bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer				
CC	with leucocyte infiltration of the skin or organs. The present sequence				
CC	is human TACI protein extracellular domain				
XX	XX				
SQ	Sequence 166 AA;				
Query Match					
Best Local Similarity		23.9%;	Score 67.5;	DB 5;	Length 166;
Matches		11;	Gaps	1;	Indels 15;



Search completed: December 21, 2005, 16:05:46  
Job time : 173.6 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:57:04 ; Search time 28.2 Seconds  
(without alignments)  
174.009 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51

Perfect score: 283

Sequence: 1 MLQWAGQCSQNEYPFSLHA.....TPPLTCQRYCNASVINSYKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR 80:\*

1: Pirl:\*

2: Pirl2:\*

3: Pirl3:\*

4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	184	2	S43486 B-cell maturation
2	70.5	24.9	1548	2	S34583 serine proteinase
3	69.5	24.6	5376	2	T42215 zonadhesin - mouse
4	68.5	24.2	1101	2	T16940 hypothetical prote
5	65.5	23.1	1239	2	T43251 furin (EC 3.4.21.7
6	62.5	22.1	999	2	T19275 hypothetical prote
7	62	21.9	330	2	T25169 gibberellin-regula
8	61.5	21.7	483	2	T24856 hypothetical prote
9	61.5	21.7	483	2	G88946 protein T12A7.2 (i
10	61.5	21.7	520	2	T13954 MEGF6 protein - xa
11	60.5	21.4	1574	2	T14119 seven-pass transme
12	60.5	21.4	3034	2	T14119 hypothetical prote
13	59.5	21.0	388	2	T31887 hypothetical prote
14	59.5	21.0	388	2	T31888 hypothetical prote
15	59.5	21.0	438	2	T31898 hypothetical prote
16	59.5	21.0	445	2	T31577 hypothetical prote
17	59	20.8	758	2	T14557 epidermal growth f
18	59	20.8	1717	1	A45558 alpha-51D immobill
19	58.5	20.7	2533	2	T28675 alpha-51D-immobill
20	58.5	20.7	2533	2	T28674 chymotrypsin/elast
21	58	20.5	63	2	S07127 hypothetical prote
22	58	20.5	1513	2	T23681 laminin alpha-4 ch
23	58	20.5	1816	1	S68960 furin (EC 3.4.21.7
24	57.5	20.3	1680	2	A43434 hypothetical prote
25	57	20.1	502	2	T20130 hypothetical prote
26	57	20.1	653	2	G96675 hypothetical prote
27	57	20.1	838	2	T20125 hypothetical prote
28	56.5	20.0	701	2	S62460 zonadhesin - pig
29	56	19.8	2476	2	T34022

30	56	19.8	2824	2	T22759	hypothetical prote
31	55.5	19.6	339	1	KHRTB	cathepsin B (EC 3.
32	55.5	19.6	378	2	B99588	protein R09F10.7 (
33	55.5	19.6	815	1	T05754	S-receptor kinase
34	55.5	19.6	989	2	T01519	hypothetical prote
35	55	19.4	294	2	T23682	hypothetical prote
36	55	19.4	339	1	KHMSB	cathepsin B (EC 3.
37	55	19.4	758	2	S46625	finger protein XuL
38	55	19.4	1620	2	T27283	hypothetical prote
39	54.5	19.3	392	2	T27303	hypothetical prote
40	54.5	19.3	419	2	S69207	membrane endothei
41	54.5	19.3	493	2	JC5486	hypothetical prote
42	54.5	19.3	879	2	C90879	hypothetical prote
43	54.5	19.3	879	2	H64888	membrane protein y
44	54.5	19.3	879	2	G85739	hypothetical prote
45	54.5	19.3	2155	2	T30197	alpha tectorin - m
46	54	19.1	282	2	I48763	siah-1A protein -
47	54	19.1	282	2	S35754	siah-1B protein -
48	54	19.1	474	2	T27297	hypothetical prote
49	54	19.1	497	2	T27827	hypothetical prote
50	54	19.1	1099	2	T16822	hypothetical prote
51	54	19.1	1980	2	S54307	myosin heavy chain
52	54	19.1	2022	2	A59256	myosin-IxB [simila
53	53.5	18.9	255	2	A84544	hypothetical prote
54	53.5	18.9	332	2	T21458	hypothetical prote
55	53.5	18.9	356	2	T21681	hypothetical prote
56	53.5	18.9	915	2	T21773	hypothetical prote
57	53.5	18.9	927	2	T21772	hypothetical prote
58	53.5	18.9	1895	2	T15881	hypothetical prote
59	53.5	18.9	1935	2	T39411	RNA helicase - fla
60	53	18.7	98	2	C89046	protein C10G8.4 (i
61	53	18.7	274	2	F86276	F14L17.2 protein -
62	53	18.7	447	2	A96639	protein Tif9.18 (i
63	53	18.7	455	1	GOHUT1	tumor necrosis fac
64	53	18.7	592	1	JCL480	protein kinase C (
65	53	18.7	596	2	F88188	protein C18H9.7 (i
66	53	18.7	654	2	T30136	hypothetical prote
67	53	18.7	712	1	VCLJSA	env polyprotein pr
68	53	18.7	859	1	VCLJST	env polyprotein pr
69	53	18.7	1034	2	JC5598	mucin - rat
70	53	18.7	1077	2	T41146	probable cysteine-
71	53	18.7	1474	2	D88550	protein ZC84.6 (lm
72	53	18.7	2844	2	S28291	hypothetical prote
73	52.5	18.6	118	2	S61051	hypothetical prote
74	52.5	18.6	378	2	T51647	myb-related trans
75	52.5	18.6	389	2	T29488	hypothetical prote
76	52.5	18.6	397	2	F72072	probable transamin
77	52.5	18.6	397	2	C86552	aspartate aminotra
78	52.5	18.6	563	2	A36054	mucin homolog - bo
79	52.5	18.6	847	2	D72860	viral capsid assoc
80	52.5	18.6	1589	2	T42233	submaxillary mucin
81	52.5	18.6	3635	2	T10053	laminin alpha 5 ch
82	52	18.4	56	2	JN0380	trypsin inhibitor
83	52	18.4	141	2	S20915	lysozyme (EC 3.2.1
84	52	18.4	180	2	PC1305	genome polyprotein
85	52	18.4	181	2	T05301	hypothetical prote
86	52	18.4	304	1	JC2264	tissue factor path
87	52	18.4	420	2	T30507	probable alkaline
88	52	18.4	547	2	T34318	hypothetical prote
89	52	18.4	689	2	T52060	protein MEDEA (lmp
90	52	18.4	852	1	VCLJGG	env polyprotein pr
91	52	18.4	869	2	S53098	envelope polyprote
92	52	18.4	1115	2	S40241	G protein-coupled
93	52	18.4	1483	2	S30015	hypothetical prote
94	52	18.4	1747	2	T43162	antimicrobial pept
95	51.5	18.2	63	2	S57816	antimicrobial - gyp
96	51.5	18.2	424	2	T14525	S-locus-specific g
97	51.5	18.2	685	2	S78040	fibulin, splice fo
98	51.5	18.2	705	2	S34968	fibulin, splice fo
99	51.5	18.2	837	2	S43656	furin (EC 3.4.21.7
100	51.5	18.2	1008	2	T15099	hypothetical prote
101	51.5	18.2	2120	2	T30243	alpha tectorin - c
102	51	18.0	166	2	H89044	protein B0238.12 (

103	51	18.0	197	2	E85068	hypothetical prote	176	49.5	17.5	775	1	EDBE11	immediate-early pr
104	51	18.0	314	2	T27686	hypothetical prote	177	49.5	17.5	858	1	JC2481	S-receptor kinase
105	51	18.0	326	1	GOVZML	T2 protein - myxom	178	49.5	17.5	861	2	A48825	Notch homolog Motc
106	51	18.0	392	2	T29519	hypothetical prote	179	49.5	17.5	1031	2	T46636	glycine dehydrogen
107	51	18.0	401	2	T32348	hypothetical prote	180	49.5	17.5	1557	2	T28811	hypothetical prote
108	51	18.0	447	2	C85085	hypothetical prote	181	49.5	17.5	1798	2	S53869	laminin beta-2 cha
109	51	18.0	463	2	T26655	hypothetical prote	182	49.5	17.5	3075	2	S14458	laminin alpha-1 ch
110	51	18.0	561	2	T27318	hypothetical prote	183	49.5	17.5	4544	1	S02392	alpha-2-macroglobu
111	51	18.0	592	1	A30314	protein kinase C (	184	49	17.3	97	2	T18173	hypothetical prote
112	51	18.0	626	2	T27319	hypothetical prote	185	49	17.3	133	2	A57005	Norrie disease can
113	51	18.0	641	2	E96612	probable transcrip	186	49	17.3	135	2	T15610	hypothetical prote
114	51	18.0	746	2	G84605	hypothetical prote	187	49	17.3	174	2	C89075	protein K04A8.9 [i
115	51	18.0	1186	2	T18210	delta endotoxin -	188	49	17.3	189	2	T48828	hypothetical prote
116	50.5	17.8	91	2	C82657	hypothetical prote	189	49	17.3	283	2	C72272	hypothetical prote
117	50.5	17.8	99	2	S60230	gibberellin-regula	190	49	17.3	306	2	B71439	hypothetical prote
118	50.5	17.8	242	2	T29699	hypothetical prote	191	49	17.3	321	1	S28390	homeotic protein m
119	50.5	17.8	249	2	T27782	hypothetical prote	192	49	17.3	340	2	S58770	cathepsin B (EC 3.
120	50.5	17.8	328	2	G89152	protein C24B5.5 [i	193	49	17.3	346	2	T20458	hypothetical prote
121	50.5	17.8	335	2	T31559	hypothetical prote	194	49	17.3	350	2	JC5828	paired-box-contain
122	50.5	17.8	352	2	S11926	cellulose 1,4-beta	195	49	17.3	425	2	T18592	hypothetical prote
123	50.5	17.8	439	2	T23627	hypothetical prote	196	49	17.3	472	1	A35327	vitamin D-binding
124	50.5	17.8	610	1	I46001	C4b-binding protei	197	49	17.3	497	2	S69544	apoptosis inhibito
125	50.5	17.8	1043	2	T13172	gag-like protein p	198	49	17.3	524	2	S47143	A mating type prot
126	50.5	17.8	1091	1	PL0009	complement C3d/Eps	199	49	17.3	600	2	T18593	hypothetical prote
127	50.5	17.8	1847	2	T30558	resistance protein	200	49	17.3	602	2	T47794	hypothetical prote
128	50	17.7	63	2	S08572	chymotrypsin/elast	201	49	17.3	662	2	A37226	glucose transport
129	50	17.7	74	2	S10332	ubiquitin / riboso	202	49	17.3	782	2	S19876	genome polyprotein
130	50	17.7	177	2	S32749	genome polyprotein	203	49	17.3	885	2	S04322	env polyprotein -
131	50	17.7	202	2	S50635	hypothetical prote	204	49	17.3	1124	1	S58388	protein-tyrosine k
132	50	17.7	314	2	S35314	transcription fact	205	49	17.3	1158	2	E86327	protein Fl8014.19
133	50	17.7	324	2	T24819	hypothetical prote	206	49	17.3	1753	2	T00350	hypothetical prote
134	50	17.7	342	2	T30370	hypothetical prote	207	49	17.3	1984	2	T13171	probable vitelloge
135	50	17.7	366	2	S40407	oleoyl-lacyl-carri	208	49	17.3	2531	2	A46019	notch-1 protein -
136	50	17.7	370	2	T37282	probable cathepsin	209	49	17.3	2616	2	A57096	nudel protein prec
137	50	17.7	376	2	C81272	steroid/thyroid ho	210	49	17.3	2704	2	S09118	G surface protein
138	50	17.7	381	2	A46358	hypothetical prote	211	49	17.3	2823	2	F87908	protein T22A3.8 [i
139	50	17.7	382	2	A12415	hypothetical prote	212	49	17.3	2823	2	T23064	hypothetical prote
140	50	17.7	417	2	G84276	imidazolone-5-prop	213	49	17.3	3033	1	GNWUJ8	genome polyprotein
141	50	17.7	437	2	S05478	properdin - mouse	214	49	17.3	3102	2	T43291	laminin alpha chai
142	50	17.7	438	2	S73608	arginine deiminase	215	49	17.3	3672	2	T23433	hypothetical prote
143	50	17.7	461	2	JC4302	tumor necrosis fac	216	49	17.3	3704	2	T37316	probable laminin a
144	50	17.7	464	2	T24011	hypothetical prote	217	49	17.3	4545	1	S25111	alpha-2-macroglobu
145	50	17.7	474	1	VVHUD	vitamin D-binding	218	48.5	17.1	63	1	T1NPB2	proteinase inhibit
146	50	17.7	513	2	D88991	protein apx-1 [imp	219	48.5	17.1	105	2	T00232	hypothetical 11.7K
147	50	17.7	552	2	T27424	hypothetical prote	220	48.5	17.1	114	2	D75422	hypothetical prote
148	50	17.7	592	2	JN0877	protein kinase C (	221	48.5	17.1	120	2	T10318	hypothetical prote
149	50	17.7	782	2	S18031	genome polyprotein	222	48.5	17.1	233	2	T34078	hypothetical prote
150	50	17.7	922	2	T23573	hypothetical prote	223	48.5	17.1	275	2	T51437	hypothetical prote
151	50	17.7	1360	2	F96596	hypothetical prote	224	48.5	17.1	318	2	A45522	variant surface gl
152	50	17.7	1423	1	I37275	death-associated p	225	48.5	17.1	332	2	T41227	hypothetical prote
153	50	17.7	1599	2	T15854	hypothetical prote	226	48.5	17.1	335	2	T31561	hypothetical prote
154	50	17.7	1797	2	A55677	laminin beta-2 cha	227	48.5	17.1	335	2	T31560	hypothetical prote
155	50	17.7	1846	2	T33079	hypothetical prote	228	48.5	17.1	364	2	JC4249	recF protein - Azo
156	50	17.7	2150	2	T32497	hypothetical prote	229	48.5	17.1	428	2	T07813	S-locus-specific g
157	49.5	17.5	155	2	D82755	conserved hypothet	230	48.5	17.1	536	2	T19488	hypothetical prote
158	49.5	17.5	216	2	G83398	probable two-compo	231	48.5	17.1	554	2	T08976	2-amino-4-hydroxy-
159	49.5	17.5	247	2	S15060	MHC class II beta	232	48.5	17.1	557	2	A48434	variant-specific s
160	49.5	17.5	249	2	T25643	hypothetical prote	233	48.5	17.1	608	1	ABONS1	serum albumin 1 pr
161	49.5	17.5	288	2	T21158	hypothetical prote	234	48.5	17.1	608	1	ABONS2	serum albumin 2 pr
162	49.5	17.5	298	2	G69532	conserved hypothet	235	48.5	17.1	729	2	T23972	hypothetical prote
163	49.5	17.5	300	2	S12143	lipoprotein-associ	236	48.5	17.1	827	2	S29955	surface glycoprote
164	49.5	17.5	315	2	D48560	immediate-early pr	237	48.5	17.1	850	1	WMBE56	infected cell prot
165	49.5	17.5	325	2	B43692	T2 protein - rabbi	238	48.5	17.1	855	1	JQ2004	env polyprotein -
166	49.5	17.5	325	2	I48765	siah-2 protein - m	239	48.5	17.1	874	2	JQ0883	genome polyprotein
167	49.5	17.5	348	2	T28623	hypothetical prote	240	48.5	17.1	878	2	AD0664	probable exported
168	49.5	17.5	349	2	D36858	gene G4R protein -	241	48.5	17.1	1126	2	S49208	transmembrane prot
169	49.5	17.5	349	2	D72175	G2R protein - vari	242	48.5	17.1	1188	2	D86236	protein Fl4N23.5 [
170	49.5	17.5	357	2	T21152	hypothetical prote	243	48	17.0	61	2	AF2219	hypothetical prote
171	49.5	17.5	396	2	S53325	tissue factor path	244	48	17.0	87	2	T00564	gibberellin-regula
172	49.5	17.5	441	2	S12707	genome polyprotein	245	48	17.0	177	2	S32746	genome polyprotein
173	49.5	17.5	575	1	VCLJHD	env polyprotein pr	246	48	17.0	177	2	S32741	genome polyprotein
174	49.5	17.5	654	2	C96782	unknown protein P2	247	48	17.0	180	2	PC1303	genome polyprotein
175	49.5	17.5	728	2	T20561	hypothetical prote	248	48	17.0	199	2	B86288	F911.31 protein -

249 48 17.0 229 2 T22037  
250 48 17.0 266 2 T46314  
251 48 17.0 271 2 A70415  
252 48 17.0 304 1 THUGK  
253 48 17.0 317 2 A39935  
254 48 17.0 331 2 T26871  
255 48 17.0 367 2 S46336  
256 48 17.0 369 2 S21471  
257 48 17.0 371 2 T22652  
258 48 17.0 431 2 G75305  
259 48 17.0 450 1 TFEVMR  
260 48 17.0 479 2 T02623  
261 48 17.0 492 2 S41288  
262 48 17.0 539 2 T01513  
263 48 17.0 572 2 T29880  
264 48 17.0 597 2 T08681  
265 48 17.0 661 2 E71427  
266 48 17.0 666 2 T30098  
267 48 17.0 681 2 B53542  
268 48 17.0 697 2 E96752  
269 48 17.0 705 1 TFCHE  
270 48 17.0 788 2 I51530  
271 48 17.0 839 2 T41826  
272 48 17.0 888 2 A54280  
273 48 17.0 962 2 JC5571  
274 48 17.0 969 1 A39490  
275 48 17.0 975 2 JC5570  
276 48 17.0 1079 1 TVFVMI  
277 48 17.0 1189 2 T42726  
278 48 17.0 1203 2 A49175  
279 48 17.0 1852 1 VJCH2  
280 48 17.0 2215 2 T00348  
281 48 17.0 2219 2 T27684  
282 48 17.0 2395 1 S50820  
283 48 17.0 4543 1 A53102  
284 47.5 16.8 131 2 S53380  
285 47.5 16.8 160 2 I84444  
286 47.5 16.8 201 2 D71190  
287 47.5 16.8 202 2 T22237  
288 47.5 16.8 297 2 T28775  
289 47.5 16.8 319 2 C81319  
290 47.5 16.8 328 2 F63351  
291 47.5 16.8 354 2 R75630  
292 47.5 16.8 355 1 S22181  
293 47.5 16.8 370 2 E82369  
294 47.5 16.8 388 2 A88949  
295 47.5 16.8 390 2 T25642  
296 47.5 16.8 411 2 T29475  
297 47.5 16.8 427 2 T07811  
298 47.5 16.8 429 2 T14535  
299 47.5 16.8 431 2 T07812  
300 47.5 16.8 477 2 AG0765

ALIGNMENTS

RESULT 1  
S43486  
B-cell maturation factor - human  
N:Alternate names: BCM protein; BEL protein  
C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S43486; S31208; S36661  
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
Nucleic Acids Res. 22, 1147-1154, 1994  
A:Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidirectional  
A:Reference number: S43486; MUID:942182235; PMID:8165126  
A:Accession: S43486  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-184 <LAA>  
A:Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:g471244; PID:

R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
EMBO J. 11, 3897-3904, 1992  
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)  
A:Reference number: S31208; MUID:93010984; PMID:1396583  
A:Accession: S31208  
A:Molecule type: mRNA  
A:Residues: 1-184 <LAA>  
A:Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:  
A:Accession: S36661  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 4-184 <LAA>  
A:Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955  
C:Genetics:  
A:Gene: GDB:BCMA  
A:Cross-references: GDB:135977; OMIM:109545  
A:Map position: 16p13.1-16p13.1  
A:Introns: 44/1; 93/1  
C:Superfamily: human B-cell maturation factor  
Query Match 100.0%; Score 283; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 8.5e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVK 51  
Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVK 51  
RESULT 2  
S34583  
serine proteinase (EC 3.4.21.-) PC6B - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S34583  
R:Nakagawa, T.; Murakami, K.; Nakayama, K.  
FEBS Lett. 327, 165-171, 1993  
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a  
A:Reference number: S34583; MUID:93327934; PMID:8335106  
A:Accession: S34583  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1548 <NAK>  
A:Cross-references: UNIPROT:Q04592; UNIPARC:UPI000016CF9E; GB:D17583; NID:g407344; PIDN:  
C:Keywords: hydrolase; serine proteinase  
Query Match 24.9%; Score 70.5; DB 2; Length 1548;  
Best Local Similarity 34.7%; Pred. No. 4.2;  
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;  
Qy 7 QCSQNEYFDSLHACIPCOLRCSSNTPP-----LTCQRYCNASVTNSVK 50  
Db 1151 ECAAVEYWDGSHRQCCHKKSCSGSPSEDQCTCPRETFLNTTCVK 1199  
RESULT 3  
T42215  
zonadhesin - mouse  
N:Alternate names: sperm-specific membrane protein  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T42215  
R:Gao, Z.; Garbers, D.L.  
J. Biol. Chem. 273, 3415-3421, 1998  
A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot  
A:Reference number: Z22080; MUID:98123114; PMID:9452463  
A:Accession: T42215  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5376 <GAO>  
A:Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:g3327420; PI  
C:Genetics:  
A:Gene: Zan

A;Map position: 5

C;Function:

A;Description: functions in multiple cell adhesion processes

A;Note: found exclusively on the apical region of the sperm head

C;Keywords: cell adhesion

Query Match 24.6%; Score 69.5; DB 2; Length 5376;

Best Local Similarity 36.8%; Pred. No. 16;

Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIP-CQLRCSNTP--PLTCQRYC 41

DB 3299 QCPNTSQFTDCLPSCVPCSNRCEVTSPSPSCREGC 3336

RESULT 4

T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T16840

R;Geiselsel, C.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid T10E10.

A;Reference number: Z18588

A;Accession: T16840

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1101 <GEI>

A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PI

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T10E10.4

A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match

Best Local Similarity 24.2%; Score 68.5; DB 2; Length 1101;

Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;

QY 7 QCSQNEYFDSLHACIPCOLR--CSSNTPLTCQRYCNASVTNSVKG 51

DB 350 QCSQSTVFNSDLNVCPLAIQNSCDSSTQQPVCS--C-SQVSSSCPG 393

RESULT 5

T43251

furin (EC 3.4.21.75) - fall armyworm

N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin

C;Species: Spodoptera frugiperda (fall armyworm)

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T43251

R;Ciemplick, M.; Klenk, H.

submitted to the EMBL Data Library, January 1996

A;Description: Cloning and functional characterization of PURIN from Spodoptera frugiper

A;Reference number: Z22368

A;Accession: T43251

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1299 <CIE>

A;Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:g1167859; PI

A;Experimental source: clone Sforin 6; ovary

C;Function:

A;Description: responsible for the endoproteolytic processing of proproteins with specif

C;Keywords: hydrolase; serine proteinase

Query Match

Best Local Similarity 23.1%; Score 65.5; DB 2; Length 1299;

Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 8 CSQNEYFDSLHACIPCOLRCS-----SNTPLTCQRYCNAS-----VTNSVKG 51

DB 1150 CSRPLRIDRLNQCVCPC---CSERGVTNSTPTDC-CHCNPNGBGNCINSSVAG 1198

RESULT 6

T19275

hypothetical protein F34D10.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T19275; T21723

R;Harris, B.

submitted to the EMBL Data Library, September 1994

A;Reference number: Z19099

A;Accession: T19275

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-999 <WIL>

A;Cross-references: UNIPROT:Q17969; UNIPARC:UPI0000079A41; EMBL:Z37139; PIDN:CAA85494.1;

A;Experimental source: clone C14B1

R;Kershaw, J.

submitted to the EMBL Data Library, June 1994

A;Reference number: Z19464

A;Accession: T21723

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-999 <W12>

A;Cross-references: UNIPARC:UPI0000079A41; EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GN00021; C

A;Experimental source: clone F34D10

C;Genetics:

A;Gene: CESP:F34D10.2

A;Map position: 3

A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870/

Query Match

Best Local Similarity 22.1%; Score 62.5; DB 2; Length 999;

Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY 13 YFDSLHACIPCOL-RCSSNTPLTCQRYCNASVTNSVKG 51

DB 516 YEDSLNTCIGRAPERVKMTPLRLIQSYFVSSTPNGLDG 555

RESULT 7

T25169

hypothetical protein T23F1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T25169

R;Wilkinson, J.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19990

A;Accession: T25169

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-330 <WIL>

A;Cross-references: UNIPROT:O18118; UNIPARC:UPI000006118C; EMBL:Z81129; PIDN:CAB03405.1;

A;Experimental source: clone T23F1

C;Genetics:

A;Gene: CESP:T23F1.6

A;Map position: 5

A;Introns: 16/3

C;Superfamily: gliadin

Query Match

Best Local Similarity 21.9%; Score 62; DB 2; Length 330;

Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

QY 8 CSQNEYFDSLHACIP-----CQLRCSNTPPL---TCQRYCNASVTN 47

DB 59 CASSQYQLQTSQCWPACQSCSQCCSQSNNTTQCQPTCCQSCQTSSCN 106

RESULT 8

S60231

giberellin-regulated protein GASA3 precursor - Arabidopsis thaliana

N;Alternate names: GAST1 protein homolog

[illegible]

T31887  
hypothetical protein C03A7.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31887  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31887  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-388 <GRE>  
A:Cross-references: UNIPROT:O16500; UNIPARC:UPI000007BC52; EMBL:AF016451; PIDN:AAB66001.1  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.4  
A:Map position: 5  
A:Introns: 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 388;  
Best Local Similarity 31.9%; Pred. No. 22;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QMAGCCSQNEYFDSLHACIPCOLRC-SSNTPLTTCORYCNASVTNS 48  
Db 316 QCAPQCEQS-----CQQQCVQQQPPAAQCQTACQSSCSNS 350

RESULT 14  
T31888  
hypothetical protein C03A7.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31888  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31888  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-388 <GRE>  
A:Cross-references: UNIPROT:O16501; UNIPARC:UPI0000077D46; EMBL:AF016451; PIDN:AAB65996.1  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.7  
A:Map position: 5  
A:Introns: 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 388;  
Best Local Similarity 31.9%; Pred. No. 22;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QMAGCCSQNEYFDSLHACIPCOLRC-SSNTPLTTCORYCNASVTNS 48  
Db 316 QCAPQCEQS-----CQQQCVQQQPPAAQCQTACQSSCSNS 350

RESULT 15  
T31889  
hypothetical protein C03A7.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31889  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31889  
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-438 <GRE>  
A:Cross-references: UNIPROT:O16502; UNIPARC:UPI000007AF62; EMBL:AF016451; PIDN:AAB65995.1  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.8  
A:Map position: 5  
A:Introns: 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 438;  
Best Local Similarity 31.9%; Pred. No. 24;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QMAGCCSQNEYFDSLHACIPCOLRC-SSNTPLTTCORYCNASVTNS 48  
Db 366 QCAPQCEQS-----CQQQCVQQQPPAAQCQTACQSSCSNS 400

RESULT 16  
T31898  
hypothetical protein C03A7.14 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31898  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31898  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-445 <GRE>  
A:Cross-references: UNIPROT:O16511; UNIPARC:UPI000007B691; EMBL:AF016451; PIDN:AAB66007.1  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.14  
A:Map position: 5  
A:Introns: 18/3; 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 445;  
Best Local Similarity 31.9%; Pred. No. 25;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QMAGCCSQNEYFDSLHACIPCOLRC-SSNTPLTTCORYCNASVTNS 48  
Db 373 QCAPQCEQS-----CQQQCVQQQPPAAQCQTACQSSCSNS 407

RESULT 17  
T15577  
hypothetical protein C23G10.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C:Accession: T15577  
R:Latreille, P.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid C23G10.  
A:Reference number: Z18372  
A:Accession: T15577  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-758 <LAT>  
A:Cross-references: UNIPROT:Q9GYR5; UNIPARC:UPI000017925B; EMBL:U39851; NID:g1055062; PII  
C:Genetics:  
A:Gene: CESP:C23G10.8  
A:Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3

Query Match 20.8%; Score 59; DB 2; Length 758;  
Best Local Similarity 42.9%; Pred. No. 44;  
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
QY 15 DSLHACIPQLRCSNTTPEL 35
Db 260 ESFVHPLYPAIRKCSADGPPL 280

RESULT 18
A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Schistosoma mansoni
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45558; S27836
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol Biochem Parasitol 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep
A;Reference number: A45558; MUID:92365727; PMID:1501637
A;Accession: A45558
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1717 <SHO>
A;Cross-references: UNIPROT:Q26566; UNIPARC:UPI000007DCD7; EMBL:M86396; NID:g160957; PID
A;Note: sequence extracted from NCBI backbone (NCBIP:111129)
C;Genetics:
A;Gene: SER
C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F;1018-1323/Domain: protein kinase homology <KIN>
F;1026-1034/Region: protein kinase ATP-binding motif

Query Match 20.8%; Score 59; DB 1; Length 1717;
Best Local Similarity 39.1%; Pred. No. 89;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 QCSONEYFDSLHACIPQLRCS 29
Db 645 ECFRNTYIDQTRHCLPCNESCS 667

RESULT 19
T28675
alpha-51D immobilization antigen - Paramesidium tetraurelia
C;Species: Paramesidium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28675
R;Schwegmann, K.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:P90589; UNIPARC:UPI0000078A73; EMBL:X96400; PIDN:CAA65264.1
C;Genetics:
A;Gene: alpha-51D
A;Genetic code: SGC5
A;Introns: 280/3; 538/2; 1248/2
C;Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGCSONEYF-----DSLHACIPQLRCSNTTPTLCQR----- 39
Db 1661 AGACTNKKCYDNVTATSDSECDSYLSGCVTRGTGTCIPNSEPCTSYRGTKLQCELFFKFTG 1720

QY 40 -----YCNASVNTSVKG 51
Db 1721 LDANKNPIYECGSDATNTATG 1742

Query Match 20.8%; Score 59; DB 1; Length 1717;
Best Local Similarity 39.1%; Pred. No. 89;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 QCSONEYFDSLHACIPQLRCS 29
Db 645 ECFRNTYIDQTRHCLPCNESCS 667

RESULT 19
T28675
alpha-51D immobilization antigen - Paramesidium tetraurelia
C;Species: Paramesidium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28675
R;Schwegmann, K.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:P90589; UNIPARC:UPI0000078A73; EMBL:X96400; PIDN:CAA65264.1
C;Genetics:
A;Gene: alpha-51D
A;Genetic code: SGC5
A;Introns: 280/3; 538/2; 1248/2
C;Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGCSONEYF-----DSLHACIPQLRCSNTTPTLCQR----- 39
Db 1661 AGACTNKKCYDNVTATSDSECDSYLSGCVTRGTGTCIPNSEPCTSYRGTKLQCELFFKFTG 1720

QY 40 -----YCNASVNTSVKG 51
Db 1721 LDANKNPIYECGSDATNTATG 1742
```

```
RESULT 20
T28674
alpha-51D-immobilization antigen - Paramesidium tetraurelia
C;Species: Paramesidium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28674
R;Schmidt, H.J.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z20505
A;Accession: T28674
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:Q27183; UNIPARC:UPI000007E3B2; EMBL:X85135; NID:g728634; PID:
C;Genetics:
A;Genetic code: SGC5
A;Note: alpha-51D
C;Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGCSONEYF-----DSLHACIPQLRCSNTTPTLCQR----- 39
Db 1661 AGACTNKKCYDNVTATSDSECDSYLSGCVTRGTGTCIPNSEPCTSYRGTKLQCELFFKFTG 1720

QY 40 -----YCNASVNTSVKG 51
Db 1721 LDANKNPIYECGSDATNTATG 1742

RESULT 21
S07127
chymotrypsin/elastase inhibitor - common roundworm
C;Species: Ascaris lumbricoideis (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S07127
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A;Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoideis: the prima
A;Reference number: S07127; MUID:84255715; PMID:6564898
A;Accession: S07127
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-63 <BAB>
A;Cross-references: UNIPARC:UPI000012D146
C;Superfamily: roundworm trypsin inhibitor

Query Match 20.5%; Score 58; DB 2; Length 63;
Best Local Similarity 36.6%; Pred. No. 6.9;
Matches 15; Conservative 5; Mismatches 13; Indels 8; Gaps 4;

QY 8 CSONEYFDSLHACIPQLRCS--SSNTP-PLTCQR-YNAS 44
Db 5 CGPNEVWTE---CTGCENKCGPDENTPCPLMCRPSCECS 41

RESULT 22
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781
A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:O17970; UNIPARC:UPI000007686D; EMBL:Z81573; PIDN:CAB04625.1;
A;Experimental source: clone M02G9
```





C/Species: Schizosaccharomyces pombe  
C/Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: T38571; S62460  
R/Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, October 1995  
A/Reference number: Z21745  
A/Accession: T38571  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-701 <BA2>  
A/Cross-references: UNIPROT:Q09807; UNIPARC:UPI000013A007; EMBL:ZS4354; NID:g1019398; PFI  
A/Experimental source: strain 972h-, cosmid c2G11  
C/Genetics:  
A/Gene: SPAC2G11.05c  
A/Map position: 1L

Query Match 20.0%; Score 56.5; DB 2; Length 701;  
Best Local Similarity 28.6%; Pred. No. 79;  
Matches 14; Conservative 12; Mismatches 18; Indels 5; Gaps 2;

Qy 4 MAGQC SQNEYFDSLL--HACIFQLRCSSNTPLTTCORYCNASVTNSVK 50  
:: :: ||| :: ||| :: ||| :: ||| :: ||| ::  
Db 87 LSSSSNERESFENLIFEHACLILYRLACTVHT---TAISLCNKKPPNLVQ 132

RESULT 29  
T34022  
zonadesin - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: T34022  
R/Hardy, D.M.; Garbers, D.L.  
J. Biol. Chem. 270, 26025-26028, 1995  
A/Title: A sperm membrane protein that binds in a species-specific manner to the egg ext  
A/Reference number: Z21464; MUID:96064658; PMID:7592795  
A/Accession: T34022  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-2476 <HAR>  
A/Cross-references: UNIPROT:Q28983; UNIPARC:UPI000013C373; EMBL:U40024; NID:g10666465; PFI  
A/Experimental source: strain Meishan; testis  
C/Genetics:  
A/Gene: Zan  
C/Function:  
A/Description: may be involved in sperm adhesion to the zona pellucida

Query Match 19.8%; Score 56; DB 2; Length 2476;  
Best Local Similarity 31.6%; Pred. No. 2,7e+02;  
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 8 CSQNEYFDSLHACIP-CQ---LRCSNTPLTTCORYC 41  
||| :: | :: ||| :: ||| :: ||| ::  
Db 1851 CSAHSVYTSCVPCLPSCQDPQGCTGAGAPSTCEGC 1888

RESULT 30  
T22759  
hypothetical protein F55H12.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T22759  
R/Dobson, R.  
submitted to the EMBL Data Library, October 1996  
A/Reference number: Z19610  
A/Accession: T22759  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-2824 <WIL>  
A/Cross-references: UNIPROT:P90891; UNIPARC:UPI000017BA22; EMBL:Z81091; PIDN:CAB03143.1  
A/Experimental source: clone F55H12  
C/Genetics:  
A/Gene: CESP:F55H12.3  
A/Map position: 1











QY 2 LQWAGCQNEYFDSLLHACIPCOLRCSSNTPTLTTCORYCNASVTNSV 49  
Db 707 LKKKGQLS-----FTPVSDAGIECHSRNSNKTPTQICDQWNVSVFVISV 750

RESULT 51  
S54307  
myosin heavy chain - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C:Accession: S54307  
R:Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Bachler, M.  
EMBO J. 14, 697-704, 1995  
A:Title: A novel type of myosin implicated in signalling by rho family GTPases.  
A:Reference number: S54307; MUID:95188874; PMID:7882973  
A:Accession: S54307  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1980 <REI>  
A:Cross-references: UNIPROT:Q63358; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:G639998; PID:  
C:Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z  
F:149-942/Domain: myosin motor domain homology <MMOT>  
F:239-246/Region: nucleotide-binding motif A (P-loop)  
F:1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 19.1%; Score 54; DB 2; Length 1980;  
Best Local Similarity 52.9%; Pred. No. 3.7e+02;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 23 PCQLRCSSNTPTLTTCOR 39  
Db 1812 PCLLRCPDNDPLTSMK 1828

RESULT 52  
A59256  
myosin-IXb [similarity] - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 31-Dec-2004  
C:Accession: A59256; I61700  
R:Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.  
J. Cell Sci. 109, 653-661, 1996  
A:Title: Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase-  
A:Reference number: A59256; MUID:97063843; PMID:8907710  
A:Accession: A59256  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-2022 <WIR>  
A:Cross-references: UNIPROT:Q14788; UNIPARC:UPI00000161189; GB:U42391; NID:g1147782; PID:  
R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.  
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994  
A:Title: Identification and overlapping expression of multiple unconventional myosin gen  
A:Reference number: A55758; MUID:94294418; PMID:8022818  
A:Accession: I61700  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 234-322 <RES>  
A:Cross-references: UNIPARC:UPI0000073918; GB:L29149; NID:G457257; PIDN:AAA20912.1; PID:  
C:Genetics:  
A:Gene: GDB:MYO9B; OMIM:602129  
A:Map position: 19p13.1  
C:Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolo  
F:149-941/Domain: myosin motor domain homology #status atypical <MMO>  
F:239-246/Region: nucleotide-binding motif A (P-loop)

Query Match 19.1%; Score 54; DB 2; Length 2022;  
Best Local Similarity 52.9%; Pred. No. 3.7e+02;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 23 PCQLRCSSNTPTLTTCOR 39  
Db 1812 PCLLRCPDNDPLTSMK 1828

Db 1852 PCLLRCPDNDPLTSMK 1868

RESULT 53  
A84544  
hypothetical protein At2g16770 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: A84544  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84544  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <STO>  
A:Cross-references: UNIPROT:Q9SLE1; UNIPARC:UPI00000A1869; GB:AE002093; NID:G4581120; PID:  
C:Genetics:  
A:Gene: At2g16770  
A:Map position: 2

Query Match 18.9%; Score 53.5; DB 2; Length 255;  
Best Local Similarity 37.2%; Pred. No. 73;  
Matches 16; Conservative 3; Mismatches 15; Indels 9; Gaps 3;

QY 4 MAGO---CSQNEYFDSLL---HACI---PCQLRCSSNTPTLTTC 37  
Db 13 MGGELPSCSMDSFFDELLRDSHACTHTTCTNPPGENTHTTTC 55

RESULT 54  
T21458  
hypothetical protein F27E5.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21458  
R:Wilkinson, J.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: Z19425  
A:Accession: T21458  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-332 <WIL>  
A:Cross-references: UNIPROT:Q09553; UNIPARC:UPI000008359F; EMBL:Z48582; PIDN:CAA88466.1;  
C:Genetics:  
A:Gene: CESP:F27E5.4  
A:Map position: 2  
A:Introns: 87/3; 101/2; 152/2; 236/1; 284/3

Query Match 18.9%; Score 53.5; DB 2; Length 332;  
Best Local Similarity 28.6%; Pred. No. 91;  
Matches 14; Conservative 6; Mismatches 20; Indels 9; Gaps 2;

QY 8 CSQNEYFDSLLHACIPCO---LRCSNTPTL-----TCORYCNASVTN 47  
Db 119 CLAQEAASEACTALTDCENLEBQCNRLAPLMAACSTNTCQPCRSAVLN 167

RESULT 55  
T21681  
hypothetical protein F32H5.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21681  
R:Steward, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19458  
A:Accession: T21681  
A:Status: preliminary; translated from GB/EMBL/DBJ







A:Residues: 1-455 <HIM>  
A:Cross-references: UNIPARC:UPI0000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:  
A:Accession: C36555  
A:Molecule type: protein  
A:Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',169-2  
A:Cross-references: UNIPARC:UPI000002D398; UNIPARC:UPI000002D836; UNIPARC:UPI00001736DE;  
A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A:Reference number: A38281; MUID:91017509; PMID:2170974  
A:Accession: A38281  
A:Molecule type: mRNA  
A:Residues: 1-455 <GRA>  
A:Cross-references: UNIPARC:UPI0000002CE11; GB:M37764  
A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
I form of the receptor.  
A:Reference number: S12057; MUID:91006021; PMID:1698610  
A:Accession: S12057  
A:Molecule type: mRNA  
A:Residues: 1-455 <NOP>  
A:Cross-references: UNIPARC:UPI0000002CE11; EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID  
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
R:Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A:Reference number: JT0758; MUID:94085779; PMID:8262379  
A:Accession: JT0758  
A:Molecule type: DNA  
A:Residues: 1-13 <MEM>  
A:Cross-references: UNIPARC:UPI0000155CFB  
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A:Reference number: A60231; MUID:90292216; PMID:2113477  
A:Accession: A60231  
A:Molecule type: protein  
A:Residues: 41-43,'X',45-53,'X',55-57 <SEC>  
A:Cross-references: UNIPARC:UPI0000072FDB  
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
tients.  
A:Reference number: A38258; MUID:91062364; PMID:2174164  
A:Accession: A38258  
A:Molecule type: protein  
A:Residues: 41-60 <GAT>  
A:Cross-references: UNIPARC:UPI00001736E1  
A:Experimental source: cancer patient serum  
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from  
A:Reference number: A60594; MUID:89171156; PMID:2924890  
A:Accession: A60594  
A:Molecule type: protein  
A:Residues: 41-43,'X',45-53,'V',55-57,'XX',60 <OLS>  
A:Cross-references: UNIPARC:UPI00001736E2  
A:Experimental source: renal failure patient urine  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:90110215; PMID:2153136  
A:Accession: A35010  
A:Molecule type: protein  
A:Residues: 41-45 <ENG>  
A:Cross-references: UNIPARC:UPI00001736E3  
A:Experimental source: normal urine  
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f

A:Reference number: JC2404; MUID:95128033; PMID:7765720  
A:Accession: JC2404  
A:Molecule type: protein  
A:Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>  
A:Cross-references: UNIPARC:UPI00001736E4  
A:Experimental source: urine  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Genetics:  
A:Gene: GDB:TNPR1  
A:Cross-references: GDB:125913; OMIM:191190  
A:Map position: 12p13.2-12p13.2  
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F:30-201/Domain: extracellular #status predicted <EXT>  
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-196/Domain: NGF receptor repeat homology <NG4>  
F:212-234/Domain: transmembrane #status predicted <MEM>  
F:235-455/Domain: intracellular #status predicted <INT>  
F:54,145,151/Binding site: carboxydrate (Asn) (covalent) #status predicted  
Query Match 18.7%; Score 53; DB 1; Length 455;  
Best Local Similarity 33.3%; Pred. No. 1.4e+02;  
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;  
QY 8 CSQNE---YFDSLHACIPCOLRCSSNTPTPLTCORYCNASVT 46  
DB 127 CRKNQRYHWSNLFQCFNCSL-CLNGTVHLSCOEKQNTVCT 167  
RESULT 64  
JC1480  
protein kinase C (EC 2.7.1.1-) zeta - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-Oct-2004  
C:Accession: JC1480  
R:Goodnight, J.; Kazanietz, M.G.; Blumberg, P.M.; Mushinski, J.F.; Mischak, H.  
Gene 122, 305-311, 1992  
A:Title: The cDNA sequence, expression pattern and protein characteristics of mouse prote  
A:Reference number: JC1480; MUID:93138400; PMID:1487145  
A:Accession: JC1480  
A:Molecule type: mRNA  
A:Residues: 1-592 <GOO>  
A:Cross-references: UNIPROT:Q02956; UNIPARC:UPI0000029ADD; GB:M94632; NID:g200498; PIDN:?  
A:Experimental source: brain  
C:Superfamily: protein kinase C, zeta/iota types; protein kinase C zinc-binding repeat  
C:Keywords: ATP; phorbol ester binding; phosphotransferase; serine/threonine-specific pr  
F:131-180/Domain: protein kinase C zinc-binding repeat homology <KZ1>  
F:250-518/Domain: protein kinase homology <KIN>  
F:258-266/Region: protein kinase ATP-binding motif  
F:281/Active site: Lys #status predicted  
Query Match 18.7%; Score 53; DB 1; Length 592;  
Best Local Similarity 34.9%; Pred. No. 1.7e+02;  
Matches 15; Conservative 8; Mismatches 14; Indels 6; Gaps 3;  
QY 6 GQCSQNEY-FDSLHACIPCOL----RCSSNTPTPLTCORYCNA 43  
DB 145 GQCSERWGLSRQGYRCINCCLKLVHKRCHV-LVPLTCRRHMS 186  
RESULT 65  
F88188  
protein C18H9.7 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: F88188  
R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes  
 A:Reference number: A75000; MUID:199069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gac/C.elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999; and  
 A:Accession: F88188  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-536 <STO>  
 A:Cross-references: UNIPROT:Q09485; UNIPARC:UPI00000816F3; GB:chr\_II; PID:g722386; GSPDB:199069613  
 C:Genetics:  
 A:Gene: C18H9.7  
 A:Map position: 2

Query Match 18.7%; Score 53; DB 2; Length 596;  
 Best Local Similarity 31.4%; Pred. No. 1.7e+02;  
 Matches 11; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 8 CSQNEFYDLSLLHACIPCOLRCSSNTPLTLCQRYCN 42  
 Db 54 CDQGEYGLSVLSQVQLATDQDSAMKCEAFLN 88

RESULT 66  
 T30136  
 hypothetical protein C14C11.8 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T30136  
 R:Du, Z.; Gattung, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Description: The sequence of *C. elegans* cosmid C14C11.  
 A:Reference number: Z20742  
 A:Accession: T30136  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-654 <DUE>  
 A:Cross-references: UNIPROT:Q17982; UNIPARC:UPI000017B77B; EMBL:U53141; PIDN:AAA96110.1;  
 A:Experimental source: strain Bristol N2; clone C14C11  
 C:Genetics:  
 A:Gene: CESP:C14C11.8  
 A:Map position: 5  
 A:Introns: 50/3; 98/3; 155/3; 182/3; 229/3; 318/3; 365/3; 522/3; 543/3; 586/3

Query Match 18.7%; Score 53; DB 2; Length 654;  
 Best Local Similarity 37.1%; Pred. No. 1.9e+02;  
 Matches 13; Conservative 5; Mismatches 15; Indels 2; Gaps 2;

QY 15 DSSLHACIPCOLRCSSNTPLTLCQRYCN 47  
 Db 532 NNCVQACQPCQCTCGSNVQCACQNSCQCGN 566

RESULT 67  
 VCLJ54  
 env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST/24.1C/2)  
 N:Alternate names: coat polyprotein  
 N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41  
 C:Species: human immunodeficiency virus type 2, HIV-2  
 A:Note: host *Homo sapiens* (man)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 R: Mulligan, M.J.; Yamshchikov, G.V.; Ritter Jr., G.D.; Gao, P.; Jin, M.J.; Nail, C.D.; S. J. Virol. 66, 3971-3975, 1992  
 A:Title: Cytoplasmic domain truncation enhances fusion activity by the exterior glycoprotein gp120  
 A:Reference number: A42535; MUID:92260681; PMID:1583738  
 A:Accession: A42535  
 A:Molecule type: DNA  
 A:Residues: 1-712 <MUL>  
 A:Cross-references: UNIPROT:P32536; UNIPARC:UPI000012A033; GB:M86924; NID:g325760; PIDN:19920681  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-712/Product: env polyprotein #status predicted <ENV>  
 F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>  
 F:506-712/Product: transmembrane glycoprotein gp41 #status predicted <TPG>  
 F:507-523/Region: hydrophobic  
 F:675-694/Domain: transmembrane #status predicted <TMN>  
 F:36,69,78,113,119,131,137,145,160,173,200,232,235,242,266,272,283,294,304,359,392,402,404,409

Query Match 18.7%; Score 53; DB 1; Length 712;  
 Best Local Similarity 29.3%; Pred. No. 2e+02;  
 Matches 12; Conservative 7; Mismatches 12; Indels 10; Gaps 1;

QY 19 HACIPCOLRCSSNT-----PPLTCQRYCNASVTNSV 49  
 Db 409 HNYVPCHIKQIINTWHKVGKNVLPREGQLTCNSTVTSII 449

## RESULT 68

VCLJST  
 env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST)

N:Alternate names: coat polyprotein  
 N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41  
 C:Species: human immunodeficiency virus type 2, HIV-2  
 A:Note: host *Homo sapiens* (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Sep-1994  
 C:Accession: H33943  
 R:Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.; J. Virol. 64, 890-901, 1990  
 A:Title: Molecular characterization of an attenuated human immunodeficiency virus type 2  
 A:Reference number: A33943; MUID:90112662; PMID:2296086  
 A:Accession: H33943  
 A:Molecule type: genomic RNA  
 A:Residues: 1-859 <KUM>  
 A:Cross-references: UNIPARC:UPI0000174A3A; EMBL:M86924  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-859/Product: env polyprotein #status predicted <ENV>  
 F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>  
 F:506-859/Product: transmembrane glycoprotein gp41 #status predicted <TPG>  
 F:507-523/Region: hydrophobic  
 F:675-694/Domain: transmembrane #status predicted <TMN>  
 F:36,69,78,113,119,131,137,145,160,173,186,200,232,235,242,266,272,283,294,304,359,392,402,409

Query Match 18.7%; Score 53; DB 1; Length 859;  
 Best Local Similarity 29.3%; Pred. No. 2.3e+02;  
 Matches 12; Conservative 7; Mismatches 12; Indels 10; Gaps 1;

QY 19 HACIPCOLRCSSNT-----PPLTCQRYCNASVTNSV 49  
 Db 409 HNYVPCHIKQIINTWHKVGKNVLPREGQLTCNSTVTSII 449

## RESULT 69

JCS598

mucin - rat

C:Species: *Rattus norvegicus* (Norway rat)  
 C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 09-Jul-2004  
 C:Accession: JCS598  
 R:Inatomi, T.; Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K. Biochem. Biophys. Res. Commun. 236, 789-797, 1997  
 A:Title: Cloning of rat Muc5AC mucin gene: Comparison of its structure and tissue distribution  
 A:Reference number: JCS598; MUID:97396181; PMID:9245735  
 A:Accession: JCS598  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA

A:Residues: 1-1034 <INA>

A:Cross-references: UNIPROT:Q35888; UNIPARC:UPI00000E7779; GB:U83139; NID:g2315984; PIDN:Q35888  
 A:Note: translation not complete  
 C:Comment: This protein is a high molecular weight glycoprotein which is a major component



RESULT 74  
T51647  
myb-related transcription factor MYB33 [imported] - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: T51647  
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Paz-Ares, J.; Weisshaar, B.  
Plant J. 16, 263-276, 1998  
A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from Arabidopsis thaliana  
A:Reference number: Z14349; MUID:9839469; PMID:9839469  
A:Accession: T51647  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-378 <KRA>  
A:Cross-references: UNIPROT:Q9ZTE7; UNIPARC:UPI00000A77EF; EMBL:AF062875; PIDN:AAC83597.  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Gene: MYB33  
A:Map position: III  
C:Keywords: transcription factor

Query Match 18.6%; Score 52.5; DB 2; Length 378;  
Best Local Similarity 23.5%; Pred. No. 1.3e+02;  
Matches 16; Conservative 9; Mismatches 20; Indels 23; Gaps 2;  
  
QY 6 GGCQNEYFDSLHACIPCOLR-----CSS-----NTPPLTCORYCN 42  
DB 136 GNCASPRYENFTPIPSKRLWSELLYPGCSSTIKQEFSSPEQFRNTSPQISKTC 195  
QY 43 ASVTNSVK 50  
DB 196 FSVPCDVE 203

RESULT 75  
T29488  
hypothetical protein M01H9.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29488  
R;Pauley, A.; Gattung, S.  
submitted to the EMBL Data Library, September 1996  
A:Description: The sequence of C. elegans cosmid M01H9.  
A:Reference number: Z20626  
A:Accession: T29488  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-389 <PAU>  
A:Cross-references: UNIPROT:Q95018; UNIPARC:UPI000007DA14; EMBL:U70853; PIDN:AAB09143.1;  
A:Experimental source: strain Bristol N2; clone M01H9  
C:Genetics:  
A:Gene: CESP:M01H9.2  
A:Map position: 4  
A:Introns: 51/1; 96/1; 121/3; 209/2; 319/1

Query Match 18.6%; Score 52.5; DB 2; Length 389;  
Best Local Similarity 34.1%; Pred. No. 1.4e+02;  
Matches 14; Conservative 5; Mismatches 15; Indels 7; Gaps 2;  
  
QY 8 CSQNEYFDSLHACI-----PCOLRCSSNTPPLTCORYCN 42  
DB 317 CSGYQCIDSIIKIDCAEVKAQAGACKLSVASBYCPRTCE-YCN 356

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RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Stomach;
RA Tomasetto C.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1; -, mRNA.
DR HSSP; P56682; 1CCV.
DR Ensembl; ENSMUSG00000048191; Mus musculus.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00216; VWD; 1.
FT NON_TER 1
FT NON_TER 499
SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 499;
Best Local Similarity 48.3%; Pred. No. 1.9;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLT 36
   |||||  |||||
DB 430 CSQNEYFDHSEGTCVPC-----APPTT 451

RESULT 8
Q80Z18 MOUSE
ID Q80Z18 MOUSE PRELIMINARY; PRT; 1674 AA.
AC Q80Z18;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted gel-forming mucin (Fragment).
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC SFRAIN=C57BL/6J;
RX PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
RA Escande F., Buisaine M.P.;
RL "The mouse secreted gel-forming mucin gene cluster.";
RT Biochim. Biophys. Acta 1676:240-250(2004).
DR EMBL; AJ511857; CAD54415.1; -, Genomic DNA.
DR EMBL; AJ511858; CAD54415.1; JOINED; Genomic_DNA.
DR HSSP; Q46162; 1KJ0.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
FT NON_TER 1674
FT NON_TER 1674
SQ SEQUENCE 1674 AA; 181168 MW; 3BC42CB004476309 CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 1674;
Best Local Similarity 48.3%; Pred. No. 6.8;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLT 36
   |||||  |||||
DB 1181 CSQNEYFDHSEGTCVPC-----APPTT 1202

RESULT 9
Q80T03 MOUSE
ID Q80T03 MOUSE PRELIMINARY; PRT; 2850 AA.

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QY      8 CSQNEVFDLHACIPQLRCSNTPLTCQRYC 41
DB      6 CPKQYWDSSRKSCVSCALTCQSRS-QRTCTDFC 38

RESULT 11
QSSU83 MOUSE
ID      QSSU83_MOUSE PRELIMINARY;      PRT;      140 AA.
AC      QSSU83;
DT      01-FEB-2005 (T-EMBLrel. 29, Created)
DT      01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT      01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE      Tumor necrosis factor receptor superfamily, member 13b
DE      (Fragment).
GN      Name=Tnfrsf13b; ORFNames=RP23-5512.2-003;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Holt K.;
RL      Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AL646093; CAI25895.1; -; Genomic DNA.
DR      GO; GO:0004872; F:receptor activity; IEA.
KW      Receptor.
FT      NON_TER      140
SQ      SEQUENCE      140 AA; 15672 MW; 005D8CDF48E3D15 CRC64;

Query Match      25.3%; Score 71.5; DB 2; Length 140;
Best Local Similarity 35.3%; Pred. No. 0.69;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY      8 CSQNEVFDLHACIPQLRCSNTPLTCQRYC 41
DB      6 CPKQYWDSSRKSCVSCALTCQSRS-QRTCTDFC 38

RESULT 12
ID      TR13B_MOUSE STANDARD;      PRT;      249 AA.
AC      Q9ET35; Q9DBZ3;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE      activator and CAML interactor).
GN      Name=Tnfrsf13b; Synonyms=Taci;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Tissue=Splice;
RC      TISSUE=Splice;
RX      MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
RA      Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT      Identification of a receptor for Blys demonstrates a crucial role in
RT      humoral immunity";
RL      Nat. Immunol. 1:37-41(2000).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX      MEDLINE=C57BL/6J; TISSUE=Lung;
RC      STRAIN=C57BL/6J; PubMed=12466851; DOI=10.1038/nature01266;
RA      Okazaki I., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA      Nikaido K., Otsu N., Sato R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA      Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA      Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA      Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA      Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA      Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

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RA      Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA      Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA      Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA      Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA      Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA      Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA      Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA      Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA      Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA      Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA      Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA      Wilming L.G., Wyszaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA      Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA      Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA      Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA      Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA      Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA      Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA      Birney E., Hayashizaki Y.;
RT      Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs";
RL      Nature 420:563-573(2002).
RN      [3]
RP      FUNCTION.
RX      MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;
RA      Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA      Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
RA      Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA      Meng S.-Y., Boyle W.J., Hsu H.;
RT      "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT      factor family member involved in B cell regulation.";
J. Exp. Med. 192:137-143(2000).
RN      [4]
RP      FUNCTION.
RX      MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;
RA      Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA      Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT      "TACI-ligand interactions are required for T cell activation and
RT      collagen-induced arthritis in mice.";
Nat. Immunol. 2:632-637(2001).
RL      Nat. Immunol. 2:632-637(2001).
CC      -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC      that binds both ligands with similar high affinity. Mediates
CC      calcineurin-dependent activation of NF-AT, as well as activation
CC      of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC      cell function and the regulation of humoral immunity (By
CC      similarity).
CC      -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC      domain of CAMLG with its C-terminus (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC      -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AF257673; AAC000081.1; -; mRNA.
DR      EMBL; AK004668; BAB23457.1; -; mRNA.
DR      Ensembl; ENSMUSG0000010142; Mus musculus.
DR      MGI; MGI:1889411; Tnfrsf13b.
DR      GO; GO:0009897; C:external side of plasma membrane; IDA.
DR      GO; GO:0005887; C:integral to plasma membrane; IDA.
DR      GO; GO:0001782; P:B cell homeostasis; IMP.
DR      GO; GO:0030889; P:negative regulation of B cell proliferation; IMP.
DR      InterPro; IPR001368; TNFR_C6.
DR      PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR      PROSITE; PS00505; TNFR_NGFR_2; FALSE_NEG.
KW      Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.
FT      TOPO_DOM      1 128
FT      Extracellular (Potential).
FT      TRANSMEM      129 149
FT      Signal-anchor for type III membrane
FT      protein (Potential).
FT      TOPO_DOM      150 249
FT      Cytoplasmic (Potential).

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PCSK5_MOUSE
ID PCSK5_MOUSE STANDARD; PRT; 1877 AA.
AC Q04592; Q62040;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Proteinkin convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Protein convertase PCS5) (Subtilisin/kexin-like protease PCS5) (PC6)
DE (Subtilisin-like proprotein convertase 6) (SPC6).
GN Name=PCSK5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RP NUCLEOTIDE SEQUENCE OF 330-1877 (ISOFORM PCS5B).
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-O;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM PCSA).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8466318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
RA Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: its striking
structural similarity to PACE4.";
RL J. Biochem. 113:132-135(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM PCSA).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lussan J., Vieau D., Hamelin J., Day R., Christien M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
RN [5]
RP PARTIAL PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;
RA De Bie T., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
RA Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PCS5 are sorted to different
subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
RN [6]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=96293359; PubMed=8698813; DOI=10.1083/jcb.134.1.181;
RA Constam D.B., Calton M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
RN [7]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=97436919; PubMed=9291583;
RX DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
CC -1- FUNCTION: Likely to represent a widespread endoprotease activity
within the constitutive and regulated secretory pathway. Capable
of cleavage at the RX(K/R)R consensus motif. May be responsible
for the maturation of gastrointestinal peptides. May be involved
in the cellular proliferation of adrenal cortex via the activation
of growth factors.
CC -1- CATALYTIC ACTIVITY: Release of mature proteins from their
proteins by cleavage of Arg-Xaa-Yaa-Arg|-Zaa bonds, where Xaa

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CC can be any amino acid and Yaa is Arg or Lys.
CC -1- SUBCELLULAR LOCATION: PCSA is secreted through the regulated
secretory pathway. PCSB is a type I membrane protein localized to
a paranuclear post-Golgi network compartment in communication with
early endosomes.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=PCSB; Synonyms=Long;
CC IsoID=Q04592-1; Sequence=Displayed;
CC Name=PCSA; Synonyms=Short;
CC IsoID=Q04592-2; Sequence=VSP_005438, VSP_005439;
CC TISSUE SPECIFICITY: PCSA is expressed in most tissues but is most
abundant in the intestine and adrenals. PCSB is expressed in the
intestine, adrenals and lung but not in the brain.
CC -1- DEVELOPMENTAL STAGE: Weakly expressed throughout the embryo,
except in the developing nervous system, the ribs and the liver,
but markedly up-regulated at discrete sites during development. At
E6.5, prominent expression observed in differentiated decidua. At
E7.5, intense expression in extraembryonic endoderm, amnion and
nascent mesoderm. At E8.5, abundant expression in somites and yolk
sac followed by a confinement to dermamyotome compartment. Between
E9.5 and E11.5, abundant expression in AER (thickened ectodermal
cells of limb buds). At E12.5, expression in the limbs is confined
to the condensing mesenchym surrounding the cartilage. At this
stage, strong expression also detected in vertebral and facial
cartilage primordia and in the muscle of the tongue. At E16.5,
abundant expression in epithelial cells of the intestinal villi.
CC Isoform A is most abundant at all stages but significant levels of
isoform B occur at E12.5.
CC -1- DOMAIN: The propeptide domain acts as an intramolecular chaperone
assisting the folding of the zymogen within the endoplasmic
reticulum.
CC -1- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain
sorting information. AC 1 directs TGN localization and interacts
with the TGN sorting protein PACS-1.
CC -1- SIMILARITY: Belongs to the peptidase S8 family.
CC -1- SIMILARITY: Contains 1 homo B/P domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; D17583; BAA04507.1; -; mRNA.
CC EMBL; D12619; BAA02143.1; -; mRNA.
CC EMBL; L14932; AAA74636.1; -; mRNA.
CC PIR; A48225; A48225.
CC PIR; S34583; S34583.
CC HSP; P23188; IP80.
CC MEROPS; S08.076; -.
CC Ensembl; ENSMUSG00000024713; Mus musculus.
CC MGI; MGI:97515; Pcsks.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0015021; C:integral to membrane; TAS.
CC InterPro; IPR003460; AFP.
CC InterPro; IPR00209; Pept_S8_S53.
CC InterPro; IPR002884; PpProtnConvertsp.
CC Pfam; PF02420; AFP; 1.
CC Pfam; PF01483; P_protein; 1.
CC Pfam; PF00082; Peptidase_S8; 1.
CC PRINTS; PD00723; SUBTILISIN.
CC ProDom; PD000717; PpProtnConvertsp; 1.
CC PROSITE; PS00136; SUBTILASE ASP; 1.
CC PROSITE; PS00137; SUBTILASE HIS; 1.
CC PROSITE; PS00138; SUBTILASE_SER; 1.
CC Alternative splicing. Cleavage on pair of basic residues;
KW Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Repeat;
KW Serine protease; Signal; Transmembrane; Zymogen.
CC SIGNAL 1 34
CC PROPEP 35 116
CC CHAIN 117 1877 Proprotein convertase subtilisin/kexin

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FT CARBOHYD 3065 3065 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3144 3144 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3172 3172 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3288 3288 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3292 3292 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3782 3782 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4005 4005 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4136 4136 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4243 4243 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4254 4254 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4335 4335 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4376 4376 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4586 4586 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 5136 5136 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 5252 5252 N-linked (GlcNAc. . .) (Potential).  
FT DISULFID 5263 5274 By similarity.  
FT DISULFID 5268 5283 By similarity.  
FT DISULFID 5285 5294 By similarity.  
SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB77DF2A2620 CRC64;

Query Match 24.6%; Score 69.5; DB 1; Length 5376;  
Best Local Similarity 36.8%; Pred. No. 54;  
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 7 QCSQNEFYDSLHACIP-CQLRCSNTP--PLTCQRYC 41  
DB 3299 QCTNSQFTDCLPSCVPCSNCRCEVTSVPSSCREGC 3336

RESULT 20  
Q22378 CASEL  
ID Q22378 CASEL PRELIMINARY; PRT; 966 AA.  
AC Q22378;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hypothetical protein T10E10.4.  
GN ORFNames=T10E10.4;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology";  
RL Science 282:2012-2018(1998).  
DR EMBL; U39644; AAA80360.2; -; Genomic\_DNA.  
DR PIR; T16840; T16840.  
DR HSSP; P10969; 1WGT.  
DR IntAct; Q22378; -  
DR Ensembl; T10E10.4; Caenorhabditis elegans.  
DR WormBase; WBGene0020421; T10E10.4.  
DR WormPep; T10E10.4; CE25989.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0006030; P:chitin metabolism; IEA.  
DR InterPro; IPR002557; Chitin bind\_Pera.  
DR InterPro; IPR006149; EB\_region.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000794; Ketoacyl synth.  
DR InterPro; IPR003571; Snake toxin.  
DR InterPro; IPR006150; Worm\_repeat\_1.  
DR Pfam; PF01607; CBM\_14; 2.  
DR Pfam; PF01683; EB; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00289; WR1; 12.  
DR PROSITE; PS00606; B\_KETOACYL SYNTHASE; UNKNOWN 1.  
DR PROSITE; PS00272; SNAKE TOXIN; UNKNOWN 1.  
KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 966 AA; 102461 MW; B565A3CDD25216D9 CRC64;  
Query Match 24.2%; Score 68.5; DB 2; Length 966;  
Best Local Similarity 36.2%; Pred. No. 12;  
Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;  
QY 7 QCSQNEFYDSLHACIPCOLR--CSSNTPPLTCQRYCNASVTNSVKG 51  
DB 215 QCSQSTVFNSDLNVCPLAIQNCDSSTQQPVC--C-SQVSSSCPG 258

RESULT 21  
Q6W4X9 HUMAN  
ID Q6W4X9 HUMAN PRELIMINARY; PRT; 1569 AA.  
AC Q6W4X9;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Mucin glycoprotein (Fragment).  
GN Name=MUC6;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;  
RA Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,  
RA Toribara N.W.;  
RT "The complete genomic organization of the human MUC6 and MUC2 mucin genes";  
RL Genomics 83:936-939(2004).  
DR EMBL; AY312160; AAQ82434.1; -; mRNA.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
DR InterPro; IPR006552; VWC\_Out.  
DR InterPro; IPR001846; VWF\_D.  
DR Pfam; PF01826; TIL; 2.  
DR Pfam; PF00094; VWD; 3.  
DR SMART; SM00215; VWC\_Out; 2.  
DR SMART; SM00216; VWD; 3.  
DR NON\_TER 1569 1569  
FT NON TER 1569 1569  
SQ SEQUENCE 1569 AA; 168065 MW; 6AEDDE143ECB855B CRC64;

Query Match 24.2%; Score 68.5; DB 2; Length 1569;  
Best Local Similarity 45.2%; Pred. No. 20;  
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEFYDSLHACIPCOLRCSNTPPLTCQ 38  
DB 1179 CSQDEYFDHEGVCFM-----PPTTPQ 1202

RESULT 22  
T13B HUMAN  
ID T13B HUMAN STANDARD; PRT; 293 AA.  
AC O14836; O7Z6F5;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).  
GN Name=TNFRSF13B; Synonyms=TACI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
RC TISSUE=B-cell;  
RX MEDLINE=97458245; PubMed=9311921; DOI=10.1126/science.278.5335.138;  
RA von Buelow G.-U., Bram R.J.;



```
RC TISSUE=Small intestine;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK223453; BAD97173.1; -; mRNA.
KW Receptor.
FT NON TER
SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;

Query Match 23.9%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.8%; Pred. No. 4.6;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYCNA 43
Db 34 CPQEWDPPLLTGCMCKTICNHQS-QRTCAAFCS 68

RESULT 24
Q6WC9 CAEBR PRELIMINARY; PRT; 135 AA.
AC Q6WC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG19174.
GN Name=CBG19174;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100098; CAE72086.1; -; Genomic_DNA.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF01826; TIL; 2.
DR PROSITE; PS01186; EGF 2; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14981 MW; 74B21060EAF539B6 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 135;
Best Local Similarity 34.8%; Pred. No. 2.4;
Matches 16; Conservative 5; Mismatches 19; Indels 6; Gaps 2;

QY 7 QCSONEYFDSLHACIP-CQLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 79 KCPQNEQRCGTACEPTCE-----NPKPMACTKQCIINVCQCAKG 119

RESULT 25
O17496 ASCSU PRELIMINARY; PRT; 532 AA.
AC O17496;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Serotonin receptor.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX Ascaris suum (Pig roundworm); PubMed=10413046; DOI=10.1016/S0166-6851(99)00059-6;
RA Huang X., Duran E., Diaz F., Xiao H., Messer W.S. Jr., Komuniecki R.;
RT "Alternative-splicing of serotonin receptor isoforms in the pharynx
RT and muscle of the parasitic nematode, Ascaris suum.";
RL Mol. Biochem. Parasitol. 101:95-106(1999).

RC TISSUE=Small intestine;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK223453; BAD97173.1; -; mRNA.
KW Receptor.
FT NON TER
SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;

Query Match 23.9%; Score 67.5; DB 2; Length 293;
Best Local Similarity 30.8%; Pred. No. 4.6;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYCNA 43
Db 34 CPQEWDPPLLTGCMCKTICNHQS-QRTCAAFCS 68

RESULT 24
Q6WC9 CAEBR PRELIMINARY; PRT; 135 AA.
AC Q6WC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG19174.
GN Name=CBG19174;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100098; CAE72086.1; -; Genomic_DNA.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF01826; TIL; 2.
DR PROSITE; PS01186; EGF 2; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14981 MW; 74B21060EAF539B6 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 135;
Best Local Similarity 34.8%; Pred. No. 2.4;
Matches 16; Conservative 5; Mismatches 19; Indels 6; Gaps 2;

QY 7 QCSONEYFDSLHACIP-CQLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 79 KCPQNEQRCGTACEPTCE-----NPKPMACTKQCIINVCQCAKG 119

RESULT 25
O17496 ASCSU PRELIMINARY; PRT; 532 AA.
AC O17496;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Serotonin receptor.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX Ascaris suum (Pig roundworm); PubMed=10413046; DOI=10.1016/S0166-6851(99)00059-6;
RA Huang X., Duran E., Diaz F., Xiao H., Messer W.S. Jr., Komuniecki R.;
RT "Alternative-splicing of serotonin receptor isoforms in the pharynx
RT and muscle of the parasitic nematode, Ascaris suum.";
RL Mol. Biochem. Parasitol. 101:95-106(1999).

[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22311325; PubMed=12423236;
RA Huang X., Xiao H., Rex E.B., Hobson R.J., Messer W.S.,
RA Komuniecki P.R., Komuniecki R.W.;
RT "Functional characterization of alternatively spliced 5-HT2 receptor
RT isoforms from the pharynx and muscle of the parasitic nematode,
RT Ascaris suum.";
RL J. Neurochem. 83:249-258(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AF005486; AAC78396.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 532 AA; 60141 MW; 4D795D1C249D5F6 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 532;
Best Local Similarity 23.8%; Pred. No. 9.9;
Matches 15; Conservative 14; Mismatches 14; Indels 20; Gaps 2;

QY 3 OMAGQCSONEYFDSLHACIPCO-----LRCSSNTPLTCQRYCNASVTN 47
Db 434 KMGVCKFGYWSN-----VSCRSRNEFVLTDRQLDNDVKTTSERPLLCGKHCNSSGN 488

QY 48 SVK 50
Db 489 SLQ 491

RESULT 26
Q54XL6 D1CDI PRELIMINARY; PRT; 574 AA.
AC Q54XL6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein DDB0230012.
GN Name=DDB0230012; ORFNames=DDB0230012;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Suggang R., Berriman M., Song J., Olsen R., Szafanski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Baeson N.,
RA Farbrother P., Desany B., Just E., Morio T., Roat R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegod H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.B., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
```

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CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AF10100053; EAL68033.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0008468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein.
SQ SEQUENCE 574 AA; 64223 MW; 9D344378077A91C8 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 574;
Best Local Similarity 35.7%; Pred. No. 11;
Matches 20; Conservative 6; Mismatches 16; Indels 14; Gaps 3;

QY 7 QCSQNEYFDS-LLHACIPQLR-----CSSNTP-----PLTCORYCNASVTNS 48
DB 359 QAKKNYIVSHLLGLTPCEDRYRESMPASSNTPSPDSRRPSPHYHNGNVNS 414

RESULT 27
Q4N599_THEPA PRELIMINARY; PRT; 1562 AA.
ID Q4N599;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE ABC transporter, putative.
DE ORFNames=TF02_0391;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]_TaxID=5875;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Perlea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Perlea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAGK0100002; EAN32674.1; -; Genomic DNA.
SQ SEQUENCE 1562 AA; 179264 MW; 44A17485D05BF8A0 CRC64;

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Query Match 23.5%; Score 66.5; DB 2; Length 1562;
Best Local Similarity 30.9%; Pred. No. 35;
Matches 17; Conservative 12; Mismatches 9; Indels 17; Gaps 4;

QY 6 GQCSQNEYF-----DSLHACIPQLCRSSNTPPLTC--QRYCNASVT 46
DB 233 GLCYRRKFFNNVKGSNVLNVCNSVLHSCSP-ESKCSN--PLYCPARRFQNSDIT 284

RESULT 28
Q55NL5_CRYNE PRELIMINARY; PRT; 861 AA.
ID Q55NL5;
AC Q55NL5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=CNBH0730;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAEO1000041; EAL19380.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 93346 MW; 8745729FBD869366 CRC64;

Query Match 23.3%; Score 66; DB 2; Length 861;
Best Local Similarity 34.8%; Pred. No. 22;
Matches 16; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

QY 6 GQCSQNEYFDSLHACIPQLCRSSNTPPLTCQRYCNASVTNSVKG 51
DB 319 GTCSSGLYDSTSSCSCSPACSTCTGPTGTSDCLSCASPRVNLQ3 364

RESULT 29
Q26489_SPOFR PRELIMINARY; PRT; 1299 AA.
ID Q26489;
AC Q26489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endoprotease FURIN.
DE Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Sf9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z68888; CAA93116.1; -; mRNA.
DR F01; T43251; T43251.
DR HSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.

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DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.  
 DR InterPro: IPR006212; Furin\_repeat.  
 DR InterPro: IPR002029; Pept S8 S53.  
 DR InterPro: IPR002884; Peptotrconvertsp.  
 DR Pfam: PF01483; P\_proprotein; 1.  
 DR Pfam: PF00082; Peptidase S8; 1.  
 DR PRINTS: PR00723; SUBTILISIN.  
 DR SMART: SM00261; FU; 10.  
 DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN\_1.  
 DR PROSITE; PS00137; SUBTILASE HIS; 1.  
 DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
 KW Protease.  
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;  
 Query Match 23.1%; Score 65.5; DB 2; Length 1299;  
 Best Local Similarity 34.0%; Pred. No. 38;  
 Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;  
 QY 8 CSQNEVFDLSLHCIPQLRCS-----SNTPTTCORYCNAS----VTNSVKG 51  
 DB 1150 CSRPLRIDRLNNQCVC---CSRGVTNSTPTTDC-CHCNPEGECINSSVAG 1198  
 RESULT 30  
 ID STAB2 HUMAN STANDARD; PRT; 2551 AA.  
 AC Q8WQ08; Q6ZMK2; Q7Z5N9; Q86UR4; Q81UG9; Q8TES1; Q9H7H7; Q9NRY3;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Stablin-2 precursor (FEEL-2 protein) (fasciclin EGF-like laminin-type  
 DE EGF-like and link domain-containing scavenger receptor-1) (FAS1 EGF-  
 DE like and X-link domain-containing adhesion molecule-2) (Hyaluronan  
 DE receptor for endocytosis) [Contains: 190 kDa form stablin-2 (190 kDa  
 DE hyaluronan receptor for endocytosis)].  
 GN Hyal-STAB2; Synonyms=FEEL2, FELL, FE2, HARE;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21818465; PubMed=11829752; DOI=10.1042/0264-6021:3620155;  
 RA Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P.,  
 RA Johansson S., Svineng G., Franke P., Kannicht C., Kzyshkowska J.,  
 RA Longati P., Velten F.W., Johansson S., Goerdts S.;  
 RT "Stablin-1 and -2 constitute a novel family of fasciclin-like  
 RT hyaluronan receptor homologues.";  
 RL Biochem. J. 362:155-164 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE. AND FUNCTION.  
 RX MEDLINE=22206516; PubMed=12077138; DOI=10.1074/jbc.M204277200;  
 RA Adachi H., Tsujimoto M.;  
 RT "FEEL-1, a novel scavenger receptor with in vitro bacteria-binding and  
 RT angiogenesis-modulating activities.";  
 RL J. Biol. Chem. 277:34264-34270 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANT PRO-510.  
 RA Park S.-Y., Kim I.-S.;  
 RT "FE2, a novel cell adhesion molecule of Fas-1 superfamily mediates  
 RT cell-cell interaction.";  
 RN Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 35-2551.  
 RC TISSUE=Spleen;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
 RA Shigatori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,  
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,  
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Mateunawa H., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45 (2004).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE OF 1136-2551, PROTEIN SEQUENCE OF 1136-1144;  
 RP 1257-1269; 1597-1605; 1623-1645; 1652-1660; 1813-1817; 1834-1843;  
 RP 1914-1918; 1953-1957; 2204-2217; 2211-2215 AND 2355-2367, AND TISSUE  
 RP SPECIFICITY.  
 RX MEDLINE=22588541; PubMed=12626425; DOI=10.1093/glycob/cwg029;  
 RA Zhou B., McGary C.T., Weigel J.A., Saxena A., Weigel P.H.;  
 RT "Purification and molecular identification of the human hyaluronan  
 RT receptor for endocytosis.";  
 RL Glycobiology 13:339-349 (2003).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE OF 1599-2551.  
 RA Tao Q., Zhang W., Cao X.;  
 RT "Molecular cloning and characterization of human FELL sharing homology  
 RT with CD44.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Hyaluronan receptor that binds to and mediates  
 CC endocytosis of hyaluronan. May serve to maintain tissue  
 CC integrity by supporting extracellular matrix turnover or it may  
 CC contribute to maintaining fluidity of bodily liquids by resorption  
 CC of hyaluronan. Binds to both Gram-positive and Gram-negative  
 CC bacteria and may play a role in defense against bacterial  
 CC infection.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in sinusoidal endothelial  
 CC cells of liver, spleen and lymph nodes.  
 CC -1- PTM: Proteolytically processed to yield a 190 kDa protein.  
 CC -1- SIMILARITY: Contains 17 EGF-like domains.  
 CC -1- SIMILARITY: Contains 7 FAS1 domains.  
 CC -1- SIMILARITY: Contains 2 laminin EGF-like domains.  
 CC -1- SIMILARITY: Contains 1 Link domain.  
 CC -1- CAUTION: Ref.4 (BAB84877) sequence differs from that shown due to  
 CC a frameshift in position 1367.  
 CC -1- CAUTION: Ref.4 (BAD18723) sequence differs from that shown due to  
 CC frameshifts in positions 240, 253, 588 and 1586.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AJ295695; CAC82105.1; -; mRNA.  
 CC EMBL; AB052958; BAC15608.1; -; mRNA.  
 CC EMBL; AY311388; AAF74958.1; -; mRNA.  
 CC EMBL; AK024503; BAB15793.1; -; mRNA.





RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14702039; DOI=10.1038/ngl1285;  
RA Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi K., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiya M., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi O., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
DR ENBL; AK092010; BAC03789.1; -; mRNA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR Pfam; PF00431; CUB; 1; GCC2\_GCC3; 3.  
DR Pfam; PF07699; GCC2\_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4E1 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 581;  
Best Local Similarity 30.8%; Pred. No. 22;  
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
QY 7 QCSQNEYFDSLHACIPCOL-----RCSNNT 32  
DB 336 QCSQGHYNTSIHRCIRCMGSIQYDFRQNFCSRCPGNT 374

RESULT 33  
Q50LY7\_ENTHI PRELIMINARY; PRT; 799 AA.  
AC Q50LY7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Protein kinase, putative (Fragment).  
GN ORFNames=650.t00003;  
OS Entamoeba histolytica HM-1:IMSS.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS.  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
RA Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS.  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
RA Guillen N.G., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,  
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
RA Fraser C.M., Hall N.;  
RT "The genome of the protist parasite Entamoeba histolytica.";  
RL Nature 433:865-868(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR ENBL; AAFB01001427; EAL42605.1; -; Genomic\_DNA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR InterPro; IPR006212; Fuxin repeat.  
DR InterPro; IPR000719; Prot Kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00261; FU; 4.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TYRK; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; transferase.  
FT NON\_TER 1  
SQ SEQUENCE 799 AA; 91662 MW; D8BFE2F2E235989E CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 799;  
Best Local Similarity 34.3%; Pred. No. 31;  
Matches 12; Conservative 6; Mismatches 14; Indels 3; Gaps 1;  
QY 7 QCSQNEYFDSLHACIPCO---LRCSNTPPLTCQ 38  
DB 136 RCODNYVDKELQSCVCSSECLTCSNKDICTCK 170

RESULT 34  
Q50Y51\_ENTHI PRELIMINARY; PRT; 802 AA.  
AC Q50Y51;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE CXC-rich protein (Fragment).  
GN ORFNames=141.t00017;  
OS Entamoeba histolytica HM-1:IMSS.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS.  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
RA Guillen N.G., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,  
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
RA Fraser C.M., Hall N.;  
RT "The genome of the protist parasite Entamoeba histolytica.";  
RL Nature 433:865-868(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

DR EMBL; AAFB01000471; EAL46536.1; -; Genomic\_DNA.  
FT NON TER  
SQ SEQUENCE 802 AA; 90126 MW; 1425BF8514DED237 CRC64;  
  
Query Match 22.8%; Score 64.5; DB 2; Length 802;  
Best Local Similarity 34.3%; Pred. No. 31;  
Matches 12; Conservative 6; Mismatches 14; Indels 3; Gaps 1;  
  
Qy 7 QCSONEYFDSLHACIPQC---LRCSSNTPPLTCQ 38  
:|::||::||::||  
Db 653 RCQDNYVDKELQSCVGSSECLTCSNKNDICFTCK 687  
:  
  
RESULT 35  
QSCZB3\_HUMAN  
ID QSCZB3 HUMAN PRELIMINARY; PRT; 852 AA.  
AC QSCZB3;  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE Hypothetical protein DRFP6868123 (Fragment).  
DN Name=DRFP68681223;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=Testis;  
RC The German cDNA Consortium;  
RA Pousta H.A., Albert B., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (FEJ-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; CR336607; CA156752.1; -, mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR InterPro; IPR006210; IRGf\_  
DR InterPro; IPR001491; Thrombomodulin.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF\_CA; 1.  
DR Pfam; PF07699; GCC2\_GCC3; 3.  
DR PRINTS; PR00907; THROMBOMODULIN.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 7.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS00026; EGF\_3; 3.  
DR PROSITE; PS01187; EGF\_CA; 3.  
KW EGF-like domain; Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 852 AA; 93812 MW; 514918C0D126C7B2 CRC64;  
  
Query Match 22.8%; Score 64.5; DB 2; Length 852;  
Best Local Similarity 30.8%; Pred. No. 33;  
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
Qy 7 QCSONEYFDSLHACIPQL-----RCSNT 32  
|||::|::|::|::|  
Db 607 QCSPGHYYNTSIHRCAWMSYQDPFRQNFCSCPFGNT 645  
|||::|::|::|::|

```

DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
SQ SEQUENCE 880 AA; 97239 MW; F0BDE6B85266FDD60 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 880;
Best Local Similarity 30.8%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLHACIPCOL-----RCSNT 32
||| : : : : :
Db 635 QCSPGHYNTSIHRCIRCANGSYQDPFRQNFCSRCPGNT 673

RESULT 37
Q61V24 CAEBR PRELIMINARY; PRT; 919 AA.
AC Q61V24;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG05036.
GN Name=CBG05036;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; CACAC01000022; CAE61236.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01607; CBM_14; 2.
DR Pfam; PF01683; EB_1.
DR SMART; SM00289; WRI_14.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 919 AA; 96816 MW; BE3EFC096CE53DFD CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 919;
Best Local Similarity 34.0%; Pred. No. 36;
Matches 16; Conservative 10; Mismatches 16; Indels 5; Gaps 3;

QY 7 QCSQNEYFDSLHACIPCOL--CSSNTPPLTCQYCNASVTNSVKG 51
||||| : : : : :
Db 163 QCSQSTVFNALSVCVPLATQNSDSTQPVCS--C-SQVSSCPG 206

RESULT 38
Q86U29 HUMAN
ID Q86U29_HUMAN PRELIMINARY; PRT; 992 AA.
AC Q86U29;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Signal peptide, CUB domain, EGF-like 3.
GN Name=SCUBE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
SCRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Pancreas;
SCRAUSBERG R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC052263; AAH52263.2; -; mRNA.
DR HSSP; P35555; 1EMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB_2.
DR InterPro; IPR000742; EGF_Ca.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00179; EGF_CA; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 6.
SQ SEQUENCE 992 AA; 109165 MW; 24093050738932E1 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 992;
Best Local Similarity 30.8%; Pred. No. 38;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLHACIPCOL-----RCSNT 32
||||| : : : : :
Db 747 QCSPGHYNTSIHRCIRCANGSYQDPFRQNFCSRCPGNT 785

RESULT 39
Q81X30 HUMAN
ID Q81X30_HUMAN PRELIMINARY; PRT; 993 AA.
AC Q81X30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CUB and EGF containing protein (Signal peptide, CUB and EGF-like
domain containing protein 3 precursor) (OrthoMPL0000016250).
GN Name=SCUBE3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

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RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugangan R., Beriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Filcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAP10100151; EAL63792.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34482 MW; 9D863B38B2007E61 CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 300;
Best Local Similarity 31.4%; Pred. No. 15;
Matches 16; Conservative 8; Mismatches 22; Indels 5; Gaps 2;

QY 1 LMQMAGCQNEYFDSLHACIP-CQLRCSN-----TPPLTCORYGNASVT 46
Db 90 LIQSMRCNQPSVFKLCSVLFPCCQLYTNKVAVPLTCYECTQSVS 140

RESULT 45
Q9G045 GIALA
ID Q9G045 GIALA PRELIMINARY; PRT; 548 AA.
AC Q9G045
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant-specific surface protein M21-1 (Fragment).
GN Names=M21-1;
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mansouri M., Ey P.L.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298862; AAC37862.1; -; Genomic_DNA.
DR HSP; O16119; IEZG.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR006210; IEGF_like.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 4.
DR PROSITE; PS00197; 2Fe2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578FE4FDA0A2CF0E CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 548;
Best Local Similarity 30.4%; Pred. No. 28;
Matches 17; Conservative 4; Mismatches 20; Indels 15; Gaps 2;

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QY 5 AGCCSQNEYFDSLHACIP-CQLRCSNTPPLTCQ-----RVCNASVTNSVK 50
Db 209 AGCCDQGTADPTTGCKPCGI-----TDCATCEYNATISQCKTCTSSNMVK 259

RESULT 46
Q68FG9 MOUSE
ID Q68FG9_MOUSE PRELIMINARY; PRT; 827 AA.
AC Q68FG9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Scube3 protein (Fragment).
DR Name=Scube3;
GN Name=Scube3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079849; AAH79849.1; -; mRNA.
DR MGI; MGI:3045253; Scube3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF07699; GCC2_GCC3; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF_CA; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00266; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 4.
KW EGF-like domain.
FT NON_TER 1
FT NON_TER 827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;
SQ SEQUENCE 827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;

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Query Match 22.4%; Score 63.5; DB 2; Length 827;  
Best Local Similarity 30.8%; Pred. No. 42;  
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLHACIPCOL-----RCSNST 32  
DB 610 QCSQPHYNTSIHRCIRCAVGSQPDPRQNFCTRCPGNT 648

RESULT 47  
Q66PV1\_MOUSE  
ID Q66PV1\_MOUSE PRELIMINARY; PRT; 993 AA.  
AC Q66PV1\_MOUSE (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Signal peptide, CUB and EGF-like domain containing protein 3 precursor.  
DE Precursor.  
GN Name=Scube3; Synonyms=SCUBE3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6;  
RA Wu B.T., Su Y.H., Tsai M.T., Wasserman S.M., Topper J.N., Yang R.B.;  
RT "A novel secreted, cell-surface glycoprotein containing multiple epidermal growth factor-like repeats and one CUB domain is highly expressed in primary osteoblasts and bones.";  
RL J. Biol. Chem. 279:37485-37490(2004).  
DR EMBL: AY639609; AAU08348.1; -; mRNA.  
DR MGI: 3045253; Scube3.  
DR GO: 0005509; F:calcium ion binding; IEA.  
DR InterPro: IPR000152; Abx\_hydroxy1\_S.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR011641; GCC2\_GCC3.  
DR InterPro: IPR006210; IEGF.  
DR Pfam: PF00431; CUB; 1.  
DR Pfam: PF00008; EGF; 5.  
DR Pfam: PF07645; EGF\_CA; 4.  
DR Pfam: PF07699; GCC2\_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 10.  
DR SMART; SM00179; EGF\_CA; 8.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 6.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 6.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 993 AA; 108983 MW; E43989ACACCC345F CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 993;  
Best Local Similarity 30.8%; Pred. No. 51;  
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLHACIPCOL-----RCSNST 32  
DB 748 QCSQPHYNTSIHRCIRCAVGSQPDPRQNFCTRCPGNT 786

RESULT 48  
Q4UE95\_THEAN  
ID Q4UE95\_THEAN PRELIMINARY; PRT; 1563 AA.  
AC Q4UE95;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE (Subtelomeric) ABC-transporter family member, putative.  
GN ORFNames=TA12925;  
OS Theileria annulata;  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
OC Theileria.  
OX NCBI\_TaxID=5874;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Ankara isolate clone C9;  
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M., Hall N., Barrell B.G.;  
RT "The chromosome 2 sequence of Theileria annulata.";  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the ABC transporter family.  
DR EMBL: CR940348; CAI74594.1; -; Genomic\_DNA.  
DR InterPro: IPR003593; AAA\_ATPase.  
DR InterPro: IPR011527; ABC\_membrane\_1.  
DR InterPro: IPR003439; ABC\_transp\_like.  
DR Pfam: PF00005; ABC\_tran; 2.  
DR SMART; SM00382; AAA; 2.  
DR PROSITE; PS00929; ABC\_TM1F; 1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; UNKNOWN\_1.  
DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 2.  
KW ATP-binding; Membrane; Nucleotide-binding; Transport.  
SQ SEQUENCE 1563 AA; 179754 MW; A6E5972F6056CEE CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 1563;  
Best Local Similarity 30.9%; Pred. No. 82;  
Matches 17; Conservative 10; Mismatches 11; Indels 17; Gaps 4;

QY 6 QCSQNEYF-----DSLHACIPCOLRCSNSTPPLTC--QRYCNASVT 46  
DB 233 GLCYRSPFNKGVNANLVNCSVLHSCSP-DSKCSN--PLLYCPARRFQNSDIT 284

RESULT 49  
TR13C\_MOUSE  
ID TR13C\_MOUSE STANDARD; PRT; 175 AA.  
AC Q9D8D0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor 3) (B-cell maturation defect).  
DE Name=Tnfrsf13c; Synonyms=Baffr, Bcmd, Br3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).  
RC STRAIN=BALB/c; TISSUE=B-cell lymphoma;  
RX MEDLINE=21442025; PubMed=1150962; DOI=10.1126/science.1061965;  
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L., Ambrose C.;  
RA "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF.";  
RT Science 293:2108-2111(2001).  
RL [2]  
RN NUCLEOTIDE SEQUENCE (ISOFORM 1), AND DISEASE.  
RC STRAIN=A/J;  
RX MEDLINE=21475520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;  
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;  
RA "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";

Cur. Biol. 11:1547-1552(2001).

[3]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

STRAIN=57BL/6J; TISSUE=Small intestine;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,

Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,

Gaestlerland T., Gariboldi M., Giessi C., Godzik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Perteza G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.O., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Yuan Z., Zavolen M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Birney E., Hayashizaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

Nature 420:563-573(2002).

[4]

FUNCTION

MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X;

Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,

Hilbert D.M., Hayes C.E., Cancro M.P.;

"Competition for BlyS-mediated signaling through Bcmd/BR3 regulates

peripheral B lymphocyte numbers.";

Cur. Biol. 11:1986-1989(2001)

-I- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BlyS.

Promotes the survival of mature B-cells and the B-cell response.

-I- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

-I- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1;

IsoId=Q9BD0-1; Sequence=Displayed;

Name=2;

IsoId=Q9BD0-2; Sequence=VSP\_006506;

TISSUE SPECIFICITY: Highly expressed in spleen and testis;

detected at lower levels in lung and thymus.

-I- DISEASE: Defects in Tnfrsf13c are a cause of severe B-cell

deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion

in the BAFF gene leading to an altered C-terminus. The mutant RNA

is not detectable. B-cell lymphopoiesis is normal, but the life

span of peripheral B-cells is much reduced.

-I- SIMILARITY: Contains 1 TNFR-Cys repeat.

-----

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the European Bioinformatics Institute. There are no restrictions on its

use as long as its content is in no way modified and this statement is not

removed.

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ENBL; AF373847; AK91827.1; -; mRNA.

ENBL; AK008142; BAB25490.1; -; mRNA.

HSSP; Q96RJ3; 10QE.

MGI; MGI:1919299; Tnfrsf13c.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0031296; P:B cell costimulation; IDA.

DR GO; GO:0001782; P:B cell homeostasis; IMP.

DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.

DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.

DR GO; GO:0042102; P:positive regulation of T cell proliferation; IDA.

DR GO; GO:0050776; P:regulation of immune response; IMP.

DR GO; GO:0031295; P:T cell costimulation; IDA.

DR InterPro; IPR001368; TNFR\_c6.

DR PROSITE; PS00852; TNFR\_NGFR\_1; FALSE\_NEG.

DR PROSITE; PS00500; TNFR\_NGFR\_2; FALSE\_NEG.

DR Alternative splicing; Glycoprotein; Immune response; Receptor;

KW Signal-anchor; Transmembrane.

FT TOPO\_DOM 1 71 Extracellular (Potential).

FT TRANSMEM 72 92 Signal-anchor for type III membrane

FT TOPO\_DOM 93 175 protein (Potential).

FT REPEAT 21 38 Cytoplasmic (Potential).

FT CARBOHYD 23 23 TNFR-Cys (incomplete).

FT DISULFID 22 35 N-linked (GlcNAc . .) (Potential).

FT DISULFID 27 38 By similarity.

FT VARSPLIC 133 143 By similarity.

FT SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 22.3%; Score 63; DB 1; Length 175;

Best Local Similarity 50.0%; Pred. No. 9.8; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 6;

QY 7 QCSQNEYFDSLHLHACIPCOL 26

DB 21 QCNQTECFDPLVRNCVSCCL 40

RESULT 50

Q8R4W8 MOUSE PRELIMINARY; PRT; 175 AA.

AC Q8R4W8

DT 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE TRAF3 binding protein.

GN Name=Tnfrsf13c;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Mizuno K., Irie S., Sato T.-A.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF350257; AAL83914.1; -; mRNA.

DR HSSP; Q96RJ3; 10QE.

DR MGI; MGI:1919299; Tnfrsf13c.

DR GO; GO:0009897; C:external side of plasma membrane; IDA.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0001782; P:B-cell homeostasis; IMP.

DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.

DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.

DR GO; GO:0042102; P:positive regulation of T-cell proliferation; IDA.

DR GO; GO:0050776; P:regulation of immune response; IMP.

SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EE93B1 CRC64;

Query Match 22.3%; Score 63; DB 2; Length 175;

Best Local Similarity 50.0%; Pred. No. 9.8;

Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 QCSQNEYFDSLHLHACIPCOL 26

DB 21 QCNQTECFDPLVRNCVSCCL 40

RESULT 51

Q678B7\_9VIRU



Q678B7\_9VIRU PRELIMINARY; PRT; 289 AA.  
Q678B7\_2004 (TrEMBLrel. 28, Created)  
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
Hypothetical protein.  
Lymphocystis disease virus - isolate China.  
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.  
NCBI\_TaxID=256729;  
[1]  
NUCLEOTIDE SEQUENCE.  
PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;  
Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;  
"Complete Genome Sequence of Lymphocystis Disease Virus Isolated from China."  
J. Virol. 78:6982-6994 (2004).  
EMBL; AY380826; AAU10940.1; -, Genomic DNA.  
GO; GO:0004872; F:receptor activity; IEA.  
InterPro; IPR006209; EGF like.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00020; TNFR\_c6; 2.  
SMART; SM00208; TNFR; 4.  
PROSITE; PS01186; EGF 2; 2.  
PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
Hypothetical protein.  
KW  
SEQUENCE 289 AA; 32691 MW; 2686114D4D5D6C3F CRC64;  
Query Match 22.3%; Score 63; DB 2; Length 289;  
Best Local Similarity 39.4%; Pred. No. 16;  
Matches 13; Conservative 1; Mismatches 19; Indels 0; Gaps 0;  
Oy 7 QCSQNEYPDSLHACIPQLRCSSNTPPLTCOR 39  
Db 79 QCRQGYYPDSSEMCFFPCSNCESSKVKVTCNR 111  
RESULT 52  
Q8CFA7\_MOUSE PRELIMINARY; PRT; 341 AA.  
Q8CFA7\_2003 (TrEMBLrel. 23, Created)  
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Germ cell specific zinc finger protein.  
Name=Zfp393; Synonyms=Gzf;  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
NUCLEOTIDE SEQUENCE.  
STRAIN=129/SV x C57BL; TISSUE=Testis;  
MEDLINE=22239718; PubMed=12351194; DOI=10.1016/S0925-4773(02)00258-7;  
Yan W., Burns K.H., Ma L., Matzuk M.M.;  
"Identification of Zfp393, a germ cell-specific gene encoding a novel zinc finger protein."  
Mech. Dev. 118:233-239 (2002).  
EMBL; AF508984; RAN31656.1; -, mRNA.  
HSSP; P08047; 1SFL.  
Ensembl; ENSMUSG00000048626; Mus musculus.  
MG1; MG1:2181068; Zfp393.  
GO; GO:0007276; P:gametogenesis; IDA.  
InterPro; IPR007087; Znf\_C2H2.  
Pfam; PF00096; zf-C2H2; 3.  
ProDom; PD0000003; Znf\_C2H2; 2.  
SMART; SM00355; Znf\_C2H2; 3.  
PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 3.  
Metal-binding; Nuclear\_protein; Zinc; Zinc-finger.  
KW  
SEQUENCE 341 AA; 38074 MW; AC82D4C0472B054C CRC64;  
SQ

Query Match 22.3%; Score 63; DB 2; Length 341;  
Best Local Similarity 28.2%; Pred. No. 19;  
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;  
Oy 7 QCSQNEYPDSLHACIPQLRCSSNTPPLTCOR 45  
Db 59 RCNREWSQLRSUPEHGVRCPQLAPFPQNYCORS 97  
RESULT 53  
Q9D351\_MOUSE PRELIMINARY; PRT; 341 AA.  
Q9D351\_2001 (TrEMBLrel. 17, Created)  
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
Mus musculus in vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420700M05 product:weakly similar to DJ67558.1 (NOVEL ZINC FINGER PROTEIN).  
Name=Zfp393;  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
NUCLEOTIDE SEQUENCE.  
STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;  
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
Carninci P., Hayashizaki Y.;  
"High-efficiency full-length cDNA cloning."  
Meth. Enzymol. 303:19-44 (1999).  
[2]  
NUCLEOTIDE SEQUENCE.  
STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;  
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gibbs C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schirl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.;  
"Functional annotation of a full-length mouse cDNA collection."  
Nature 409:685-690 (2001).  
[3]  
NUCLEOTIDE SEQUENCE.  
STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;  
The FANTOM Consortium,  
The RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
Nature 420:563-573 (2002).  
[4]  
NUCLEOTIDE SEQUENCE.  
STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;  
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
Genome Res. 10:1617-1630 (2000).  
RL

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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sani N., Ishii Y., Nakamura S., Hazama M., Nishine T., Haraada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK018361; BAB31177.1; -; mRNA.
DR HSP; P08047; ISP1.
DR Ensembl; ENSMUSG00000048626; Mus musculus.
DR MGI; MG1:2181068; Zfp393.
DR GO; GO:0007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF000096; zf-C2H2; 2.
DR ProDom; PD000003; Znf_C2H2; 3.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.
KW SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFPC CRC64;
SQ
Query Match 22.3%; Score 63; DB 2; Length 341;
Best Local Similarity 28.2%; Pred. No. 19;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
QY 7 QCSQNEVFDLLHACIPQCLRCSSNTPPLTCQRYCNASV 45
DB 59 RCNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYCQRSI 97
RESULT 54
Q6P233_MOUSE
ID Q6P233_MOUSE PRELIMINARY; PRT; 341 AA.
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Zinc finger protein 393.
GN Name=Zfp393;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madañ A., Rodriguez S., Sanchez A.,
RA Whiting M., Madañ A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RG NIH MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064748; AAH64748.1; -; mRNA.
DR Ensembl; ENSMUSG00000048626; Mus musculus.
DR MGI; MG1:2181068; Zfp393.
DR GO; GO:0007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF000096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.
KW SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;
SQ
Query Match 22.3%; Score 63; DB 2; Length 341;
Best Local Similarity 28.2%; Pred. No. 19;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
QY 7 QCSQNEVFDLLHACIPQCLRCSSNTPPLTCQRYCNASV 45
DB 59 RCNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYCQRSI 97
RESULT 55
Q5JSG7_HUMAN
ID Q5JSG7_HUMAN PRELIMINARY; PRT; 1560 AA.
AC Q5JSG7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Proteolysin convertase subtilisin/kexin type 5 (Fragment).
GN Name=PCSK5; ORFName=RP11-422N19.4-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mashreghi-Mohammadi M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peck A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL391868; CAI40675.1; -; Genomic DNA.
DR EMBL; AL589653; CAI40809.1; -; Genomic DNA.
DR EMBL; AL353607; CAI41234.1; -; Genomic DNA.

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DR EMBL; AL353607; CAI40675.1; JOINED; Genomic DNA.
DR EMBL; AL353607; CAI40809.1; JOINED; Genomic DNA.
DR EMBL; AL589653; CAI40675.1; JOINED; Genomic DNA.
DR EMBL; AL391868; CAI40809.1; JOINED; Genomic DNA.
DR EMBL; AL391868; CAI41234.1; JOINED; Genomic DNA.
DR EMBL; AL589653; CAI41234.1; JOINED; Genomic DNA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003460; APP.
DR InterPro; IPR005560; DUF326.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR006210; IREG.
DR InterPro; IPR002029; Pept_S8_S53.
DR InterPro; IPR002884; PpPrtnConvertSP.
DR Pfam; PF02420; APP; 1.
DR Pfam; PF03860; DUF326; 2.
DR Pfam; PF01483; P_protein; 1.
DR ProDom; PD000717; PpPrtnConvertSP; 1.
DR SMART; SM00181; EGF; 16.
DR SMART; SM00261; FU; 22.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
FT NON_TER 1
SQ SEQUENCE 1560 AA; 173890 MW; 7211FBC127A8A08C CRC64;

Query Match 22.3%; Score 63; DB 2; Length 1560;
Best Local Similarity 32.6%; Pred. No. 94;
Matches 14; Conservative 6; Mismatches 21; Indels 1; Gaps 1;

QY 7 QCSQNEFYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSV 49
Db 1154 KCSFSEWDEAPGCKPCHVKFCFMCMPAEQD-CQTCPMNSL 1194

RESULT 56
Q4UHW4 THEAN PRELIMINARY; PRT; 974 AA.
AC Q4UHW4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphatephosphodiesterase
DE (EC 3.1.4.11)
GN ORFNames=TA06965;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Bartell B.G.;
RT "The chromosome 1 sequence of Theileria annulata.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
KW Hydrolase.
SQ SEQUENCE 974 AA; 110873 MW; 054988BA23DBAE41 CRC64;

Query Match 22.1%; Score 62.5; DB 2; Length 974;
Best Local Similarity 29.2%; Pred. No. 67;
Matches 14; Conservative 9; Mismatches 24; Indels 1; Gaps 1;

QY 3 QMAGQCSQNEFYFDSLHACIPQLRCSSNT-PPLTCQRYCNASVTNSV 49
Db 488 QLGGASASSIAEALLRGCRFELCDQDQSEEPVLCHAKNCHLTGTV 535

RESULT 57
Q8IZ06 HUMAN PRELIMINARY; PRT; 985 AA.
ID Q8IZ06;
AC Q8IZ06;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC26979.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC032835; AAH32835.1; -; mRNA.
DR Ensembl; ENSG00000164953; Homo sapiens.
DR InterPro; IPR000150; Hypothet_cof.
DR PROSITE; PS01228; COF_1; UNKNOWN 1.
SQ SEQUENCE 985 AA; 110872 MW; 971B5626C726B3B4 CRC64;

Query Match 22.1%; Score 62.5; DB 2; Length 985;
Best Local Similarity 21.4%; Pred. No. 67;
Matches 12; Conservative 10; Mismatches 15; Indels 19; Gaps 1;

QY 3 QMAGQCSQNEFYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSV 39
Db 34 QQPEKCDNNQYFDISALSCVPCGANQRDARGTSCVCLPGFQMISNNGGPAITCK 89

RESULT 58
Q7Z5T8 HUMAN PRELIMINARY; PRT; 985 AA.
ID Q7Z5T8 HUMAN PRELIMINARY;
AC Q7Z5T8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC26979.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RESULT 60
ID Q17969 CAEBL PRELIMINARY; PRT; 999 AA.
AC Q17969; Q19998;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein F34D10.2.
GN ORFNames=F34D10.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditiidae; Feloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN PEPTIDE SEQUENCE.
RP STRAIN=Bristol N2;
RA Harris B.R.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RX The C. elegans sequencing consortium;
RG "genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z37139; CAAB5494.1; -; Genomic DNA.
DR EMBL; Z34799; CAAB4320.1; -; Genomic DNA.
DR EMBL; Z34799; CAAB5494.1; JOINED; Genomic DNA.
DR EMBL; Z37139; CAAB4320.1; JOINED; Genomic DNA.
PIR; T19275; T19275.
DR Ensemble1; F34D10.2; Caenorhabditis elegans.
DR WormBase; WBGene0009372; F34D10.2.
DR WormPep; F34D10.2; CE01570.
DR GO; GO:006270; F:DNA replication initiation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR003874; CDC45 like.
DR Pfam; PF02724; CDC45; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 999 AA; 114888 MW; 8B46AAEB375357C9 CRC64;
Query Match 22.1%; Score 62.5; DB 2; Length 999;
Best Local Similarity 42.5%; Pred.No. 68;
Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps
Qy 13 YFDLSLLHLCIPCOL-RSSNTPLTCORYCNASVTNSVGK 51                             :   :
Dy 516 YEDSLSKTCIGRAFVRVKMTPLRLIQSYFVSSTPNGLDG 555                             :   :
RESULT 61
Q51ED6 ENTHI PRELIMINARY; PRT; 1917 AA.
AC Q51ED6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protein kinase, putative.
GN ORFNames=10.t00040;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson J., Davies R., Alsmark U.C., Samuelson J.,
RA Anedoo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Sun B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jaqels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.





Db 2224 QCDHQYQDK--NGCLPCSTECNG-----CYTVGNNCIN 2256

RESULT 65

GA3A3 ARATH STANDARD; PRT; 99 AA.

AC P46687

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Gibberellin-regulated protein 3 precursor

GN Name=GA3A3; OrderedLocNames=At4G09600; ORFNames=T35P22.40;

OS Arabidopsis thaliana (Mouse-ear cress)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI\_TaxID=3702;

[1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=cv. Columbia. TISSUE=Seed;

RX MEDLINE=95244835; PubMed=7727751;

RA Herzog M., Dorne A.-M., Grellet F.;

RT "GASA", a gibberellin-regulated gene family from Arabidopsis thaliana

RT related to the tomato GAST1 gene.;

RL Plant Mol. Biol. 27:743-752 (1995).

[2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=cv. Columbia;

RC MEDLINE=20083488; PubMed=10617196; DOI=10.1038/47134;

RX Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

RA Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Mueller M.,

RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Schmidheini T.,

RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schimidheini T.,

RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,

RA Weitzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

RA De Keyser A., Buyschaert C., Gielens J., Villarroel R., De Clercq R.,

RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,

RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,

RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,

RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,

RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,

RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

RA Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,

RA Perez-Perez A., Fumelle B., Bent E., Johnson S., Tacon D., Jesse T.,

RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,

RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,

RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,

RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,

RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,

RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,

RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,

RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,

RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,

RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,

RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,

RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;

RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis

thaliana.;"

RL Nature 402:769-777 (1999).

[3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=cv. Columbia;

RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;

RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,

RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

RA Satou M., Tamse R., Vaysberg M., Wellender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

RT "Empirical analysis of transcriptional activity in the Arabidopsis

genome.;"

RL Science 302:842-846 (2003).

CC -i- FUNCTION: Involved in late stages of seed maturation, or in early

CC steps of germination.

CC -i- SUBCELLULAR LOCATION: Secreted.

CC -i- TISSUE SPECIFICITY: Siliques and dry seeds.

CC -i- PTM: Six disulfide bonds may be present.

CC -i- SIMILARITY: Belongs to the GAST1 family.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC

CC EMBL: U11764; AAB06308.1; -; mRNA.

CC EMBL: AL161515; CAB78083.1; -; Genomic DNA.

CC EMBL: AL161831; CAB82127.1; -; Genomic DNA.

CC EMBL: AY052302; AAK96495.1; -; mRNA.

CC PIR: S60231; S60231.

CC InterPro: IPR003854; GASA.

CC Pfam: PF02704; GASA; 1.

CC Multigene family; Signal.

CC SIGNAL 1 18

CC CHAIN 19 99

CC SEQUENCE 99 AA; 10705 MW; 84549B74B08A47FA CRC64;

CC

Query Match 21.7%; Score 61.5; DB 1; Length 99;

Best Local Similarity 35.6%; Pred. No. 8.3;

Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;

Qy 6 GQCQNEYFDLLHACIPQLRCSSNTPTLTCCQRY----CNASVT 46

Db 47 GRCSKSRPNLCGRACSCCVCRCNC-VPPGTAGNHHLCPVCASIT 90

RESULT 66

Q8S258 DROME

ID Q8S258 DROME PRELIMINARY; PRT; 353 AA.

AC Q8S258;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE P162222p.

GN ORFNames=CG7348;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

[1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Berkley;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

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RA  Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA  George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA  Miranda A., Mungall C.J., Nuncio K., Pacleb J., Paragas V., Park S.,
RA  Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA  Celniker S.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AY071103; AAL48725.1; -; mRNA.
DR  Ensembl: CG7348; Drosophila melanogaster.
DR  FlyBase: FBgn0036940; CG7348.
DR  GO: GO:0005576; C:extracellular region; IEA.
DR  GO: GO:0008061; F:chitin binding; IEA.
DR  GO: GO:0006030; P:chitin metabolism; IEA.
DR  InterPro: IPR002557; Chitin_bind_Pera.
DR  Pfam: PF01607; CBM_14; 4.
DR  SMART: SM00494; ChCBD2; 3.
DR  PROSITE: PS0940; CHIT BIND II; 4.
SQ  SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;

Query Match      21.7%; Score 61.5; DB 2; Length 353;
Best Local Similarity 28.1%; Pred. No. 31;
Matches 16; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

QY  7 QCSQNEYFDLLHACIPQQL-----RCSSNTP-----PLTCQRY--CNASVTNSVK 50
Db  118 KCSVGNVFDPRARACLPVAISAHAHQCSVLDPNATLANPSCDCTYFRCHSGQAEIVQ 174

RESULT 67
Q9VW81.DROME
ID  Q9VW81.DROME PRELIMINARY; PRT; 353 AA.
AC  Q9VW81.
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  CG7348-PA.
GN  Names=CG7348; ORFNames=CG7348;
OS  Drosophila melanogaster (fruit fly)
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA  Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wassman D.A., Weinstein G.M., Weisenbach J.,
RA  Williams S.M., Wootton T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22426065; PubMed=12537568;
RA  Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA  Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA  George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA  Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA  Svirkas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA  Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT  "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT  melanogaster euchromatic genome sequence.";
RL  Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22426070; PubMed=12537573;
RA  Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA  Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA  Ashburner M., Celniker S.E.;
RT  "The transposable elements of the Drosophila melanogaster euchromatin:
RT  a genomics perspective.";
RL  Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN  [4]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review.";
RL  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN  [5]
RP  NUCLEOTIDE SEQUENCE.
RG  Berkeley Drosophila Genome Project;
RA  Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA  Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA  Yu C., Rubin G.;
RT  "Drosophila melanogaster release 4 sequence.";
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  NUCLEOTIDE SEQUENCE.
RG  FlyBase;
RL  Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AE003514; AAF49068.1; -; Genomic DNA.
DR  Ensembl: CG7348; Drosophila melanogaster.
DR  FlyBase: FBgn0036940; CG7348.
DR  GO: GO:0005576; C:extracellular region; IEA.
DR  GO: GO:0008061; F:chitin binding; IEA.
DR  GO: GO:0006030; P:chitin metabolism; IEA.
DR  InterPro: IPR002557; Chitin_bind_Pera.
DR  Pfam: PF01607; CBM_14; 4.
DR  SMART: SM00494; ChCBD2; 3.
DR  PROSITE: PS0940; CHIT BIND II; 4.
SQ  SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;

Query Match      21.7%; Score 61.5; DB 2; Length 353;
Best Local Similarity 28.1%; Pred. No. 31;
Matches 16; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

QY  7 QCSQNEYFDLLHACIPQQL-----RCSSNTP-----PLTCQRY--CNASVTNSVK 50

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Db 118 KCSVNFDPPARRACLPVAISAHQCSCVLPDNATLANPSDCETFRCHSGQAEVLQ 174
RESULT 68
Q61LZ9 CAEBR
ID Q61LZ9 CAEBR PRELIMINARY; PRT; 432 AA.
AC Q61LZ9, 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG08690.
GN Name=CBG08690;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium.
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAC0100037; CAB54085.1; -; Genomic_DNA.
DR InterPro; IPR009475; DUF1096.
DR InterPro; IPR003341; DUF139_Cys_rich.
DR Pfam; PF02363; C triplex; 10.
DR Pfam; PF06493; DUF1096; 1.
KW Hypothetical protein.
SQ SEQUENCE 432 AA; 46913 MW; CIDBALE739E9B5F6 CRC64;
Query Match 21.7%; Score 61.5; DB 2; Length 432;
Best Local Similarity 31.9%; Pred. No. 38;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;
Oy 3 QMACQCSQNEYFDSLHACIPQLRC-SSNTPPLTCORYCNASVTNS 48
Db 361 QCASQCEQS-----CQCCVQQQPPAAQCQTACQSCSNS 395
RESULT 69
Q22423 CAEBL
ID Q22423 CAEBL PRELIMINARY; PRT; 483 AA.
AC Q22423;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T12A7.2.
GN ORFNames=T12A7.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z73911; CAA98142.2; -; Genomic_DNA.
DR PIR; G88846; G88846.
DR PIR; T24856; T24856.
DR HSP; P00750; ITPG.
DR Ensembl; T12A7.2; Caenorhabditis elegans.
DR WormBase; WBGene00011723; T12A7.2.
DR WormPep; T12A7.2; CE23979.
DR InterPro; IPR00742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; 3.
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Db	132	CNSTQLFDSTWNNGSNNTEGNDTIILPCRIKQIINNWKVKAMVTPPTSGQIRCSSNI	191
Qy	46	TNSV 49	
Db	192	TGLI 195	
RESULT 73			
Q4NR8	TETNG		
AC	Q4NR8	TETNG PRELIMINARY;	PRT; 354 AA.
DT	13-SEP-2005	(TREMBlrel. 31, Created)	
DT	13-SEP-2005	(TREMBlrel. 31, Last sequence update)	
DT	13-SEP-2005	(TREMBlrel. 31, Last annotation update)	
DE	Chromosome 2	SCAF15010, whole genome shotgun sequence.	
DE	(Fragment).		
GN	ORFNames=GSTENG00031440001;		
OS	Tetraodon nigroviridis	(Green puffer).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Tetraodon.		
OX	NCBI_TaxID=99883;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE		
RA	Jailion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,		
RA	Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,		
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,		
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,		
RA	Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,		
RA	Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,		
RA	Cruaud G., Duprat S., Brottier P., Coutanceau J.P., Gouzay J.,		
RA	Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,		
RA	Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,		
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,		
RA	Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,		
RA	Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,		
RT	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals		
RT	the early vertebrate proto-karyotype."		
RL	Nature 431:946-957(2004).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE		
RG	Genoscope; Whitehead Institute Centre for Genome Research;		
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
CC	!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL: CAAE01015010; CAG09964.1; -; Genomic_DNA.		
FT	NON_TER 1 354		
FT	NON_TER 354 354		
SQ	SEQUENCE 354 AA; 39608 MW; CBEE4C670F2BDC03 CRC64;		
Query Match 21.6%; Score 61; DB 2; Length 354;			
Best Local Similarity 30.6%; Pred. No. 36;			
Matches 15; Conservative 7; Mismatches 21; Indels 6; Gaps 2;			
Qy	3	QMACGCSQNEYFDSLLHACIPQLRCSSNTPTLTQRYCNASVTNSVKG 51	
Db	279	QFCGCLNRYGEEVRDALLDPEWRC----PP--CRGTCNGCFRCARDG 321	
RESULT 74			
Q4ZLE4	PSESY		
ID	Q4ZLE4	PSESY PRELIMINARY;	PRT; 815 AA.
AC	Q4ZLE4		
DT	13-SEP-2005	(TREMBlrel. 31, Created)	
DT	13-SEP-2005	(TREMBlrel. 31, Last sequence update)	
DE	Hypothetical protein.		
GN	ORFNames=Peyr 5001;		
OS	Pseudomonas syringae	pv. syringae B728a.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
Query Match 21.4%; Score 60.5; DB 2; Length 339;			
Best Local Similarity 31.8%; Pred. No. 39;			
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;			
Qy	8	CSQNEYFDSLLHACIPQLRCSSNTPTLTQRYCNASVTNSVKG 51	
Db	108	CMNDGYNFTLGRGV-----CTSNVGEHCIFRCNSGVNKTSG 146	
Search completed: December 21, 2005, 16:10:48			

OX	NCBI_TaxID=205918;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE		
RC	STRAIN=B728a;		
RG	DOE Joint Genome Institute;		
RA	Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,		
RA	Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Dettler J.C.,		
RA	Land M., Richardson P.M., Kyripides N.C., Ivanova N.;		
RT	"Comparison of two complete genome sequences of Pseudomonas syringae		
RT	pv. syringae B728a and pv. tomato DC3000."		
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE		
RC	STRAIN=B728a;		
RA	Loper J.;		
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE		
RC	STRAIN=B728a;		
RA	Feil H., Feil W.S., Lindow S.E.;		
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: CP000075; AAY40028.1; -; Genomic_DNA.		
KW	Hypothetical protein.		
SQ	SEQUENCE 815 AA; 90781 MW; 8A638679CAF477D6 CRC64;		
Query Match 21.6%; Score 61; DB 2; Length 815;			
Best Local Similarity 30.4%; Pred. No. 85;			
Matches 17; Conservative 9; Mismatches 22; Indels 8; Gaps 2;			
Qy	4	MAGCSQNEYFDSLL-----HACIPQLRCSSNTPTLTQCO---RYCNASVTNSVKG 51	
Db	10	LAGNGSSAEWDDALPHFQHQHVPLELPGFGNPPQPCEDLASAYADALLATVKG 65	
RESULT 75			
Q61S18	CAEBR		
ID	Q61S18	CAEBR PRELIMINARY;	PRT; 339 AA.
AC	Q61S18;		
DT	25-OCT-2004	(TREMBlrel. 28, Created)	
DT	25-OCT-2004	(TREMBlrel. 28, Last sequence update)	
DT	25-OCT-2004	(TREMBlrel. 28, Last annotation update)	
DE	Hypothetical protein CBG06165		
GN	Names=CBG06165;		
OS	Caenorhabditis briggsae.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6238;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE		
RG	The C. briggsae Sequencing Consortium;		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: CAAC01000028; CAE62124.1; -; Genomic_DNA.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR006209; EGF-like.		
DR	InterPro; IPR006210; IEGF.		
DR	SMART: SM00181; EGF_2.		
DR	PROSITE; PS00022; EGF_1; 3.		
DR	PROSITE; PS01186; EGF_2; 1.		
DR	PROSITE; PS00026; EGF_3; 1.		
KW	EGF-like domain; Hypothetical protein.		
FT	NON_TER 339		
SQ	SEQUENCE 339 AA; 37704 MW; 2469B38E5B995B43 CRC64;		
Query Match 21.4%; Score 60.5; DB 2; Length 339;			
Best Local Similarity 31.8%; Pred. No. 39;			
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;			
Qy	8	CSQNEYFDSLLHACIPQLRCSSNTPTLTQRYCNASVTNSVKG 51	
Db	108	CMNDGYNFTLGRGV-----CTSNVGEHCIFRCNSGVNKTSG 146	

Job time : 191.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 16:11:46 ; Search time 5.6 Seconds

(without alignments)  
43.302 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41

Perfect score: 201

Sequence: 1 CSQNEFDLSLLHACIFCOLRCSSTPTLCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	40	US-10-967-527A-9	Sequence 9, Appli
2	201	100.0	184	US-10-742-634-9	Sequence 9, Appli
3	201	100.0	184	US-10-967-527A-8	Sequence 8, Appli
4	136	67.7	185	US-10-967-527A-10	Sequence 10, Appli
5	71.5	35.6	249	US-10-967-527A-21	Sequence 21, Appli
6	66.5	33.1	48	US-10-967-527A-20	Sequence 20, Appli
7	66.5	33.1	292	US-10-967-527A-19	Sequence 19, Appli
8	66.5	33.1	293	US-10-742-634-7	Sequence 7, Appli
9	59.5	29.6	897	US-11-137-465-35	Sequence 35, Appli
10	59.5	29.6	993	US-11-137-465-36	Sequence 36, Appli
11	58	28.9	175	US-10-967-527A-7	Sequence 7, Appli
12	53.5	26.6	5405	US-11-108-172-1116	Sequence 1116, Ap
13	50	24.9	161	US-11-126-126-2	Sequence 2, Appli
14	50	24.9	455	US-11-182-946-3	Sequence 3, Appli
15	50	24.9	909	US-11-076-187-4	Sequence 4, Appli
16	49.5	24.6	997	US-11-113-424-37	Sequence 37, Appli
17	49	24.4	42	US-10-967-527A-18	Sequence 18, Appli
18	49	24.4	231	US-11-132-285-61	Sequence 61, Appli
19	49	24.4	297	US-10-967-527A-17	Sequence 17, Appli
20	48	23.9	49	US-10-967-527A-15	Sequence 15, Appli
21	48	23.9	447	US-10-967-527A-14	Sequence 14, Appli
22	47.5	23.6	1798	US-10-995-561-1033	Sequence 1033, Ap
23	47.5	23.6	1798	US-10-995-561-1034	Sequence 1034, Ap
24	47	23.4	349	US-11-182-946-13	Sequence 13, Appli
25	47	23.4	3690	US-10-995-561-1016	Sequence 1016, Ap

Sequence 1015, Ap  
Sequence 1076, Ap  
Sequence 4, Appli  
Sequence 2, Appli  
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Sequence 22, Appli  
Sequence 50, Appli  
Sequence 57, Appli  
Sequence 35, Appli  
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Sequence 36, Appli  
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Sequence 16, Appli  
Sequence 76, Appli  
Sequence 12, Appli  
Sequence 186, Appli  
Sequence 272, Appli  
Sequence 937, Appli  
Sequence 1340, Ap  
Sequence 466, Appli  
Sequence 228, Appli  
Sequence 1412, Ap  
Sequence 7, Appli  
Sequence 142, Appli  
Sequence 62, Appli  
Sequence 213, Appli  
Sequence 10, Appli  
Sequence 827, Appli  
Sequence 825, Appli  
Sequence 836, Appli  
Sequence 1081, Ap  
Sequence 41, Appli  
Sequence 86, Appli  
Sequence 94, Appli  
Sequence 556, Appli  
Sequence 184, Appli  
Sequence 10, Appli  
Sequence 1504, Ap  
Sequence 78, Appli  
Sequence 6, Appli  
Sequence 1390, Ap  
Sequence 17, Appli  
Sequence 6, Appli  
Sequence 5478, Ap  
Sequence 5, Appli  
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Sequence 16, Appli  
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Sequence 6, Appli  
Sequence 219, Appli  
Sequence 691, Appli  
Sequence 688, Appli  
Sequence 1133, Ap  
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Sequence 408, Appli  
Sequence 297, Appli  
Sequence 30, Appli  
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Sequence 423, Appli  
Sequence 895, Appli





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; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 184
; ORGANISM: homo sapiens
US-10-967-527A-8

Query Match
Best Local Similarity 100.0%; Score 201; DB 6; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSNTTPTLTQRYC 41

RESULT 4
US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

Query Match
Best Local Similarity 67.7%; Score 136; DB 6; Length 185;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 5
US-10-967-527A-21
; Sequence 21, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

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Query Match
Best Local Similarity 35.6%; Score 71.5; DB 6; Length 249;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTQRYC 34
Db 6 CPKQYWDSSRRKSCVSCALTCQRS-QRTCTDFC 38

RESULT 6
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-20

Query Match
Best Local Similarity 33.1%; Score 66.5; DB 6; Length 48;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTQRYC 34
Db 13 CPREQYDPELLGTGCMSCKNHQS-QRTCAAFC 45

RESULT 7
US-10-967-527A-19
; Sequence 19, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 292
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-19

Query Match
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Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLTQRYC 34

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Query Match 28.9%; Score 58; DB 6; Length 175;  
Best Local Similarity 47.4%; Pred. No. 0.35;  
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CSQNEFYDLSLLHACIPCOL 19  
DB 22 CNGTECFDPLVRNCVSEL 40

## RESULT 12

US-11-108-172-1116  
; Sequence 1116, Application US/11108172  
; Publication No. US20050260177A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Smith, Carole L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick Thomas S.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.471C15  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 10/025,380  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 09/922,217  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 09/833,263  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 09/649,811  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 09/609,448  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 09/575,251  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 09/519,444  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: US 09/504,629  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: US 09/480,321  
; PRIOR FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: US 09/476,296  
; PRIOR FILING DATE: 1999-12-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1116  
; LENGTH: 5405  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-108-172-1116

Query Match 26.6%; Score 53.5; DB 7; Length 5405;  
Best Local Similarity 34.3%; Pred. No. 26;  
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEFYDLSLLHACIPCOLRCSNTPPLTCQRYC 34  
DB 2733 CPQNSHYE-----LCADTCSLGSALSAPLQCPDGC 2763

## RESULT 13

US-11-126-126-2  
; Sequence 2, Application US/11126126  
; Publication No. US20050250696A1  
; GENERAL INFORMATION:  
; APPLICANT: Fisher F., Eric  
; APPLICANT: Edwards K., Carl  
; APPLICANT: Kieft L., Gary  
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and  
; TITLE OF INVENTION: Type-II Receptors  
; FILE REFERENCE: 02-006-A  
; CURRENT APPLICATION NUMBER: US/11/126.126  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: 09/882,735  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 09/214,613  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: PCT/US97/12244  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: 60/039,792  
; PRIOR FILING DATE: 1997-03-04  
; PRIOR APPLICATION NUMBER: 60/039,314  
; PRIOR FILING DATE: 1997-02-07  
; PRIOR APPLICATION NUMBER: 60/037,737  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: 60/032,534  
; PRIOR FILING DATE: 1996-12-06  
; PRIOR APPLICATION NUMBER: 60/021,443  
; PRIOR FILING DATE: 1996-07-09  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-11-126-126-2

Query Match 24.9%; Score 50; DB 7; Length 161;  
Best Local Similarity 35.3%; Pred. No. 3.5;  
Matches 12; Conservative 5; Mismatches 13; Indels 4; Gaps 2;

QY 1 CSQNE---YFDSLHACIPCOLRCSNTPPLTCQ 31  
DB 87 CRKNQRYHWSENLPQCFNCSL-CLNGTWHLSQ 119

## RESULT 14

US-11-182-946-3  
; Sequence 3, Application US/11182946  
; Publication No. US20050255100A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280004  
; CURRENT APPLICATION NUMBER: US/11/182,946  
; CURRENT FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: US/10/186,643  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US/09/573,986  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-11-182-946-3

Query Match 24.9%; Score 50; DB 7; Length 455;  
Best Local Similarity 35.3%; Pred. No. 8.6;



```
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-61

Query Match      24.4%; Score 49; DB 7; Length 231;
Best Local Similarity 47.6%; Pred. No. 6.5;
Matches 10; Conservative 3; Mismatches 6; Indels 6; Gaps 2;

QY 1 CSONEYFDSLHACIPQCLRC 21
   | : ||| : | | : | |
Db 3 CQENEYWDQ-WGRCVTCQ-RC 21

RESULT 19
US-10-967-527A-17
; Sequence 17, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 297
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-17

Query Match      24.4%; Score 49; DB 6; Length 297;
Best Local Similarity 47.6%; Pred. No. 8.1;
Matches 10; Conservative 3; Mismatches 6; Indels 6; Gaps 2;

QY 1 CSONEYFDSLHACIPQCLRC 21
   | : ||| : | | : | |
Db 3 CQENEYWDQ-WGRCVTCQ-RC 21

RESULT 20
US-10-967-527A-15
; Sequence 15, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
```

```
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 49
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(49)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-15

Query Match      23.9%; Score 48; DB 6; Length 49;
Best Local Similarity 30.0%; Pred. No. 2.3;
Matches 9; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTC 30
   | : ||| : | | : | |
Db 7 CGENEYNYQTTGLCQECPPCGFGEPYLS 36

RESULT 21
US-10-967-527A-14
; Sequence 14, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 447
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-14

Query Match      23.9%; Score 48; DB 6; Length 447;
Best Local Similarity 30.0%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTC 30
   | : ||| : | | : | |
Db 31 CGENEYNYQTTGLCQECPPCGFGEPYLS 60

RESULT 22
US-10-995-561-1033
; Sequence 1033, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1033
; LENGTH: 1798
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1033

Query Match      23.6%; Score 47.5; DB 6; Length 1798;
Best Local Similarity 26.4%; Pred. No. 60;
Matches 14; Conservative 4; Mismatches 10; Indels 25; Gaps 3;

Qy 1 CSQNEYFDSL-----HACIP-----COL-RCSSNTPPL 28
Db 943 CHODEYSQQIVCHCRAGYTLGRCEACAPGHGDFSPRGRGRCQLCECSGNIDPM 995

RESULT 23
US-10-995-561-1034
; Sequence 1034, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1034
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1034

Query Match      23.6%; Score 47.5; DB 6; Length 1798;
Best Local Similarity 26.4%; Pred. No. 60;
Matches 14; Conservative 4; Mismatches 10; Indels 25; Gaps 3;

Qy 1 CSQNEYFDSL-----HACIP-----COL-RCSSNTPPL 28
Db 943 CHODEYSQQIVCHCRAGYTLGRCEACAPGHGDFSPRGRGRCQLCECSGNIDPM 995

RESULT 24
US-11-182-946-13
; Sequence 13, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-13

Query Match      23.4%; Score 47; DB 7; Length 349;
Best Local Similarity 43.5%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

Qy 2 SQNEYFDSLHACIPQLRCSSN 24
Db 2 SQNEYFDSLHACIPQLRCSSN 24
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Db 75 SRNNH-----LPACLSCNCRCSN 93

RESULT 25
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match      23.4%; Score 47; DB 6; Length 3690;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 15; Indels 18; Gaps 2;

Qy 1 CSQNEYFD---SLHACIPCO-----LRCSSNTPPLTCOR 32
Db 1845 CAPGFYRDVKGLFGRCPQCQCHGHSRCLPGSGVCDQCHNTEGAHCR 1894

RESULT 26
US-10-995-561-1015
; Sequence 1015, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match      23.4%; Score 47; DB 6; Length 3714;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 15; Indels 18; Gaps 2;

Qy 1 CSQNEYFD---SLHACIPCO-----LRCSSNTPPLTCOR 32
Db 1846 CAPGFYRDVKGLFGRCPQCQCHGHSRCLPGSGVCDQCHNTEGAHCR 1895

RESULT 27
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
```

PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: 08/999,811
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-11-153-880-2

Query Match      23.1%; Score 46.5; DB 7; Length 419;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 12; Conservative 2; Mismatches 19; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYC 34
Db 328 CGANREFDENTCQCV-CKRTCPRNQPLNPGKACAC 362

RESULT 31
US-11-064-774A-22
; Sequence 22, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
; FILE REFERENCE: 28967/35977B2
; CURRENT FILING DATE: 2005-02-24
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-22

Query Match      23.1%; Score 46.5; DB 7; Length 419;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 12; Conservative 2; Mismatches 19; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYC 34
Db 328 CGANREFDENTCQCV-CKRTCPRNQPLNPGKACAC 362

RESULT 32
US-11-147-047-50
; Sequence 50, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
```

```
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-50

Query Match      23.1%; Score 46.5; DB 7; Length 487;
Best Local Similarity 23.7%; Pred. No. 26;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQC-----LRCSNT 25
Db 242 CSPGHYNTTTHRCIRCPVGTQYQFPGQNHCTCPGNT 279

RESULT 33
US-10-770-726-57
; Sequence 57, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-57

Query Match      23.1%; Score 46.5; DB 6; Length 883;
Best Local Similarity 30.3%; Pred. No. 44;
Matches 10; Conservative 3; Mismatches 17; Indels 3; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRC---SSNTPPLTC 30
Db 235 CLDTVHFGRQASKCLECQVMCHPKCSTCLPATC 267

RESULT 34
US-11-113-424-35
; Sequence 35, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
```

; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 961  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-113-424-35

Query Match 23.1%; Score 46.5; DB 7; Length 961;  
Best Local Similarity 23.7%; Pred. No. 47;  
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY 1 CSQNEFDSLHACIPQ-----LRCSNT 25  
DB 743 CSPGHYNTTTHRCIRCPVGTQYQPEFGQNHCTCPGNT 780

## RESULT 35

US-11-137-465-58  
; Sequence 58, Application US/11137465  
; Publication No. US2005025558A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdock, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall, F.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Kabnick, Karen  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50018  
; CURRENT APPLICATION NUMBER: US/11/137,465  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/239,663  
; PRIOR FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: PCT/US01/09226  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/192,158  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 58  
; LENGTH: 964  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-137-465-58

Query Match 23.1%; Score 46.5; DB 7; Length 964;  
Best Local Similarity 23.7%; Pred. No. 47;  
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

.QY 1 CSQNEFDSLHACIPQ-----LRCSNT 25

DB 743 CSPGHYNTTTHRCIRCPVGTQYQPEFGQNHCTCPGNT 780

## RESULT 36

US-11-113-424-2  
; Sequence 2, Application US/11113424  
; Publication No. US20050260713A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/11/113,424  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 965  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-113-424-2

Query Match 23.1%; Score 46.5; DB 7; Length 965;  
Best Local Similarity 23.7%; Pred. No. 47;  
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY 1 CSQNEFDSLHACIPQ-----LRCSNT 25  
DB 744 CSPGHYNTTTHRCIRCPVGTQYQPEFGQNHCTCPGNT 781

## RESULT 37

US-11-147-047-51  
; Sequence 51, Application US/11147047  
; Publication No. US2005026068A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdock, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Xiang, Zhaoying  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50016  
; CURRENT APPLICATION NUMBER: US/11/147,047  
; CURRENT FILING DATE: 2005-06-07  
; PRIOR APPLICATION NUMBER: US/10/221,097  
; PRIOR FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: PCT/US01/07143  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/187,107  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: 60/236,874  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/188,916  
; PRIOR FILING DATE: 2000-03-13



```
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-51

Query Match      23.1%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 47;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQ-----LRCSSNT 25
Db      743 CSPGHYNTTTHRCIRCPVGTQPEFGKNCVSCPGNT 780

RESULT 38
US-11-080-991-50
; Sequence 50, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-50

Query Match      23.1%; Score 46.5; DB 7; Length 997;
Best Local Similarity 23.7%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQ-----LRCSSNT 25
Db      752 CSPGHYNTTTHRCIRCPVGTQPEFGKNCVSCPGNT 789

RESULT 39
US-11-113-424-36
; Sequence 36, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
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; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 999
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-36

Query Match      23.1%; Score 46.5; DB 7; Length 999;
Best Local Similarity 23.7%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQ-----LRCSSNT 25
Db      754 CSPGHYNTTTHRCIRCPVGTQPEFGKNCVSCPGNT 791

RESULT 40
US-11-078-735-12
; Sequence 12, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-078-735-12

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy      12 HACIPCOLRCSNTPPLTCQRYC 34
Db      12 HLELQIRVRCDENYVSATCNKFC 34

RESULT 41
US-11-078-735-13
; Sequence 13, Application US/11078735
; Publication No. US20050261477A1
```

```
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-13

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 42
US-11-078-735-14
; Sequence 14, Application US/11/078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-15

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 43
US-11-078-735-15
; Sequence 15, Application US/11/078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-15

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 44
US-11-132-285-41
; Sequence 41, Application US/11/132285
; Publication No. US2005024876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11PI
; CURRENT APPLICATION NUMBER: US/11/132,285
```

```
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-15

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 44
US-11-132-285-41
; Sequence 41, Application US/11/132285
; Publication No. US2005024876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11PI
; CURRENT APPLICATION NUMBER: US/11/132,285
```

```

; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, ZhaoYing
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-43

Query Match      22.9%; Score 46; DB 7; Length 1062;
Best Local Similarity 36.4%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 4; Gaps

QY      17  COLRC---SSNTPPLTCQRYC 34
      |||||      :|||:|
Db      954  CNLRCLWLWGCSIPFFSCEDLC 975

RESULT 47
US-11-078-735-21
; Sequence 21, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-21

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Page 17

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? Sequence 12, Application US/11054385
? Publication No. US20050257291A1
? GENERAL INFORMATION:
?
? APPLICANT: MIZUTANI, Masako
? APPLICANT: TANAKA, Yoshikazu
? APPLICANT: KUSUMI, Takaaki
? APPLICANT: SAITO, Kazuki
? APPLICANT: YAMAZAKI, Mami
? APPLICANT: ZHIZHONG, Gong
? TITLE OF INVENTION: GENES ENCODING PROTEINS HAVING TRANSGLYCOSYLATION
? TITLE OF INVENTION: ACTIVITY
? FILE REFERENCE: 001560-350
? CURRENT APPLICATION NUMBER: US/11/054,385
? CURRENT FILING DATE: 2005-02-10
? PRIOR APPLICATION NUMBER: US/09/147,955
? PRIOR FILING DATE: 1999-03-24
? PRIOR APPLICATION NUMBER: PCT/JP98/03199
? PRIOR FILING DATE: 1998-07-16
? PRIOR APPLICATION NUMBER: JP 9-200571
? PRIOR FILING DATE: 1997-07-25
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 12
? LENGTH: 468
? TYPE: PRT
? ORGANISM: Petunia hybrida
? US-11-054-385-12

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Query Match	Score 45;	DB 7;	Length 468;
Best Local Similarity	22.4%	Pred. No. 39;	
Matches	53.3%	1: Mismatches	6: Indels
8: Conservative			0: Gaps

Qy	19	LRCSSNTPEPLTCORY	33
		:	:
Dh	97	LTCSENGOPITCLLY	111

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RESULT 52
US-10-689-742-186
; Sequence 186, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-186

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Query Match	22.1%	Score 44.5	DB 6	Length 320
Best Local Similarity	33.3%	Pred. No. 33		
Matches 13	Conservative	1	Mismatches 16	Indels 9
				Gaps 1

Qy	5	EYFDSLLHACIPCOLRCSNTPPLT-----CQRYC	34
Dh	16	EAFDSVIGPTASCHRACOLTYPLHTYKREELVACORG	74

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RESULT 53
US-10-131-826A-272
; Sequence 272, Application US/10131826A
; Publication No. US20050245730A1
;
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;
; FILE REFERENCE: F3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
;
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
;
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
;
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
;
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
;
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
;
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
;
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
;
; SEQ ID NO 272
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-272

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Query Match	22.1%	Score 44.5	DB 6	Length 323
Best Local Similarity	33.3%	Pred. No. 33		
Matches 13; Conservative 1; Mismatches 16; Indels 9; Gaps 1;				
QY	5	EYFDSLHACIPQCLRCSSNTPLLT-----CQRYC	34	
	26	FARISVLCGDSACHPACQITVPIHTYKRELVACQGGC	74	

RESULT 54  
US-10-821-234-937  
; Sequence 937, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tanq, Y. Tom

```
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 937
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-937

Query Match      22.1%; Score 44.5; DB 6; Length 332;
Best Local Similarity 33.3%; Pred. No. 34;
Matches 13; Conservative 1; Mismatches 16; Indels 9; Gaps 1;

QY 5 EYEDSLHACIPQLRCSSNTPLT-----CORYC 34
Db 44 EAPDSVLGDTASCHRAQLTYPLHTYPEKEELYACQRC 82

RESULT 55
US-10-821-234-1540
; Sequence 1540, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1540
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1540

Query Match      21.9%; Score 44; DB 6; Length 304;
Best Local Similarity 28.9%; Pred. No. 37;
Matches 11; Conservative 7; Mismatches 16; Indels 4; Gaps 2;

QY 1 CSONE---YFDSLHACIPQLR-CSSNTPLTTCQRYC 34
Db 226 CRANENRYNSVIGKCRPKFYKCGCGNENNTSKQEC 263

RESULT 56
US-10-131-826A-466
; Sequence 466, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guernsey, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
```

```
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 466
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-466

Query Match      21.9%; Score 44; DB 6; Length 437;
Best Local Similarity 42.1%; Pred. No. 50;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 14 CIPQLRCSSNTPLTTCQR 32
Db 328 CVQPLGTCSSGSPRMTCPR 346

RESULT 57
US-11-186-284-228
; Sequence 228, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029F2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
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; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-196-284-228

Query Match      21.9%; Score 44; DB 7; Length 514;
Best Local Similarity 42.1%; Pred. No. 57;
Matches      8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Qy      12 HACIPCOL--RCSNTPPL 28
Db      262 HACIACRIIYRSDEHPPI 280

RESULT 58
US-10-821-234-1412
; Sequence 1412, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1412
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1412

Query Match      21.9%; Score 44; DB 6; Length 703;
Best Local Similarity 27.3%; Pred. No. 75;
Matches      9; Conservative 2; Mismatches 12; Indels 10; Gaps 1;

Qy      1 CSQNEYPSLLHACIPCOLRCSNTPPLTCQRY 33
Db      384 CKTYGYFDGISMCMVDVN-----ECQRY 406

RESULT 59
US-11-067-121-7
; Sequence 7, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondaal, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1028
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-067-121-7

Query Match      21.9%; Score 44; DB 7; Length 1028;

; NUMBER OF SEQ ID NOS: 44.0%; Pred. No. 1e+02;
; Matches 11; Conservative 3; Mismatches 9; Indels 2; Gaps 2;

Qy      8 DSSLHA-CIPCOLRCSN-NTPLTC 30
Db      826 DSCTHCYCLQGQTLCTVSCPLPDC 850

RESULT 60
US-10-131-826A-142
; Sequence 142, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-142

Query Match      21.9%; Score 44; DB 6; Length 1036;
Best Local Similarity 44.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 2; Gaps 2;

Qy      8 DSSLHA-CIPCOLRCSN-NTPLTC 30
Db      835 DSCTHCYCLQGQTLCTVSCPLPDC 859

RESULT 61
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Matches 13; Conservative 4; Mismatches 9; Indels 14; Gaps 2;	
Qy 1 CSQNEYF-----DSLHACIPQLRCSSNTPPLTCQRYC 34	
Db 867 CNDNLDIFSIPGCDLSGLSCLICK-----PGTTGRYC 898	
RESULT 66	
US-10-995-561-826	
; Sequence 826, Application US/10995561	
; Publication No. US20050272054A1	
; GENERAL INFORMATION:	
; APPLICANT: CARGILL, Michele et al.	
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH	
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF	
; TITLE OF INVENTION: DETECTION AND USES THEREOF	
; FILE REFERENCE: CL001559	
; CURRENT APPLICATION NUMBER: US/10/995,561	
; CURRENT FILING DATE: 2004-11-24	
; NUMBER OF SEQ ID NOS: 85702	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 826	
; LENGTH: 3116	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
US-10-995-561-826	
Query Match 21.9%; Score 44; DB 6; Length 3116;	
Best Local Similarity 32.5%; Pred. No. 2.7e+02;	
Matches 13; Conservative 4; Mismatches 9; Indels 14; Gaps 2;	
Qy 1 CSQNEYF-----DSLHACIPQLRCSSNTPPLTCQRYC 34	
Db 867 CNDNLDIFSIPGCDLSGLSCLICK-----PGTTGRYC 898	
RESULT 67	
US-10-821-234-1081	
; Sequence 1081, Application US/10821234	
; Publication No. US20050255114A1	
; GENERAL INFORMATION:	
; APPLICANT: Labat, Ivan	
; APPLICANT: Stache-Crain, Birgit	
; APPLICANT: Andarmani, Susan	
; APPLICANT: Tang, Y. Tom	
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia	
; FILE REFERENCE: 821A	
; CURRENT APPLICATION NUMBER: US/10/821,234	
; CURRENT FILING DATE: 2004-04-07	
; PRIOR APPLICATION NUMBER: US 60/462,047	
; PRIOR FILING DATE: 2003-04-07	
; NUMBER OF SEQ ID NOS: 1704	
; SOFTWARE: pt_seq_genes Version 1.0	
; SEQ ID NO 1081	
; LENGTH: 347	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
US-10-821-234-1081	
Query Match 21.6%; Score 43.5; DB 6; Length 347;	
Best Local Similarity 30.2%; Pred. No. 48;	
Matches 13; Conservative 4; Mismatches 11; Indels 15; Gaps 3;	
Qy 6 YFDSLHACIP-----COLRCSS--NTPPLTCQRYC 34	
Db 139 YLDVYL-SCVPRKAQLQLGAVCMVLASKLRETTPLTIEKLC 180	
RESULT 68	
US-11-067-121-16	
; Sequence 16, Application US/11067121	
; Publication No. US20050261185A1	
; GENERAL INFORMATION:	
; APPLICANT: Martijn, Cecile	
; APPLICANT: Rondahl, Lena	
; TITLE OF INVENTION: THERAPEUTIC PROTEINS	
; FILE REFERENCE: 18909-002001	
; CURRENT APPLICATION NUMBER: US/11/067,121	
; CURRENT FILING DATE: 2005-02-25	
; PRIOR APPLICATION NUMBER: US 60/576,445	
; PRIOR FILING DATE: 2004-06-02	
; PRIOR APPLICATION NUMBER: SE 0400489-1	
; PRIOR FILING DATE: 2004-02-27	
; NUMBER OF SEQ ID NOS: 20	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 16	
; LENGTH: 757	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
US-11-067-121-16	
Query Match 21.6%; Score 43.5; DB 7; Length 757;	
Best Local Similarity 35.0%; Pred. No. 93;	
Matches 7; Conservative 5; Mismatches 7; Indels 1; Gaps 1;	
Qy 12 HACIPQLRCSSNTPPLTCQ 31	
Db 134 HPCFP-RVRCINTSPGFRCE 152	
RESULT 69	
US-11-186-284-41	
; Sequence 41, Application US/11186284	
; Publication No. US20050266493A1	
; GENERAL INFORMATION:	
; APPLICANT: Millennium Pharmaceuticals, Inc.	
; APPLICANT: Berger, Allison	
; APPLICANT: Guillemette, Tracy L.	
; APPLICANT: Kamatkar, Shubhangi	
; APPLICANT: Schlegel, Robert	
; APPLICANT: Monahan, John E.	
; APPLICANT: Thibodeau, Stephen N.	
; APPLICANT: Burgart, Lawrence J.	
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND	
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND	
; TITLE OF INVENTION: THERAPY OF COLON CANCER	
; FILE REFERENCE: MP01-029P2RNM	
; CURRENT APPLICATION NUMBER: US/11/186,284	
; CURRENT FILING DATE: 2005-07-21	
; PRIOR APPLICATION NUMBER: US/10/301,822	
; PRIOR FILING DATE: 2002-11-21	
; PRIOR APPLICATION NUMBER: US 60/339,971	
; PRIOR FILING DATE: 2001-12-10	
; PRIOR APPLICATION NUMBER: US 60/361,978	
; PRIOR FILING DATE: 2002-03-05	
; PRIOR APPLICATION NUMBER: US 60/381,988	
; PRIOR FILING DATE: 2002-05-20	
; NUMBER OF SEQ ID NOS: 228	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 41	
; LENGTH: 757	
; TYPE: PRT	
; ORGANISM: Homo Sapiens	
US-11-186-284-41	
Query Match 21.6%; Score 43.5; DB 7; Length 757;	
Best Local Similarity 35.0%; Pred. No. 93;	
Matches 7; Conservative 5; Mismatches 7; Indels 1; Gaps 1;	
Qy 12 HACIPQLRCSSNTPPLTCQ 31	
Db 134 HPCFP-RVRCINTSPGFRCE 152	
RESULT 70	
US-10-131-826A-86	

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; Sequence 86, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 86
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-86

Query Match      21.4%; Score 43; DB 6; Length 224;
Best Local Similarity 36.0%; Pred. No. 38;
Matches 9; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

QY      10  LLHACIPQLRCSSTNPPLTCQRYC 34
Db      42  LLPAC--CPVRAQNDTEPIVLEGKC 64

RESULT 71
US-11-080-991-94
; Sequence 94, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
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; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 2214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-94

Query Match      21.4%; Score 43; DB 7; Length 2214;
Best Local Similarity 27.6%; Pred. No. 2,7e+02;
Matches 8; Conservative 5; Mismatches 8; Indels 8; Gaps 1;

QY      14  CIPQCLRCSSNT-----PPLTCQRYC 34
Db      1211 CIPQWACDGDTCQDGSDEDFVNCCKC 1239

RESULT 72
US-10-995-561-556
; Sequence 556, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 4655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-556

Query Match      21.4%; Score 43; DB 6; Length 4655;
Best Local Similarity 26.2%; Pred. No. 5.2e+02;
Matches 11; Conservative 6; Mismatches 17; Indels 8; Gaps 1;

QY      1  CSQNEYFDSLHACIPQLRC-----SSNTPLTCQRYC 34
Db      3512 CSSTQFLCANNEKCIPIWVKCDGQKDCSDGDELALCPQRFC 3553

RESULT 73
US-11-113-424-184
; Sequence 184, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gaugolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
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; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 184
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-11-113-424-184

Query Match      21.1%; Score 42.5; DB 7; Length 126;
Best Local Similarity 45.0%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 2;

Qy      14 CIP--CQLRCSSNTPPLTCQ 31
      |:|:|:|:|:|:|:|:|:|
Db      92 CLPPCCVVC---TPPTCCQ 108

RESULT 74
US-10-846-172A-10
; Sequence 10, Application US/10846172A
; Publication No. US20050257285A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Gupta, Goutam
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pierce's Disease
; FILE REFERENCE: S-102,340
; CURRENT APPLICATION NUMBER: US/10/846.172A
; CURRENT FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein
US-10-846-172A-10

Query Match      21.1%; Score 42.5; DB 6; Length 160;
Best Local Similarity 38.1%; Pred. No. 33;
Matches 8; Conservative 2; Mismatches 6; Indels 5; Gaps 1;

Qy      12 HACIPCQLRCSSNTPPLTCQR 32
      |:|:|:|:|:|:|:|:|:|
Db      114 HTCv-----CEFNCAPLSCGR 129

RESULT 75
US-10-821-234-1504
; Sequence 1504, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1504
; LENGTH: 419
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1504

Query Match      21.1%; Score 42.5; DB 6; Length 419;
Best Local Similarity 40.5%; Pred. No. 75;
Matches 15; Conservative 2; Mismatches 11; Indels 9; Gaps 3;

Qy      4 NEYFDSLHA-----CIPCQLR--CSSNTPPLTCQRY 33
      |:|:|:|:|:|:|:|:|:|
Db      190 NSGFDVLCHALESYTTLPHYHLRSPCPSPN--PITRPAY 224

Search completed: December 21, 2005, 16:30:56
Job time : 6.6 secs
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247 51.5 25.6 136 5 US-10-970-713-302 Sequence 302, Appl  
248 51.5 25.6 149 4 US-10-467-020-26 Sequence 26, Appl  
249 51.5 25.6 149 4 US-10-437-963-181538 Sequence 181538,  
250 51.5 25.6 156 4 US-10-467-020-29 Sequence 29, Appl  
251 51.5 25.6 269 4 US-10-425-115-222468 Sequence 222468,  
252 51.5 25.6 298 4 US-10-108-260A-2712 Sequence 2712, Ap  
253 51.5 25.6 298 4 US-10-679-246-2 Sequence 2, Appl  
254 51.5 25.6 365 5 US-10-846-374B-12 Sequence 12, Appl  
255 51.5 25.6 800 6 US-11-097-143-13068 Sequence 13068, A  
256 51.5 25.6 915 4 US-10-369-493-6570, Ap Sequence 6570, Ap  
257 51.5 25.6 915 4 US-10-369-493-6572 Sequence 6572, Ap  
258 51.5 25.6 927 4 US-10-369-493-6569 Sequence 6569, Ap  
259 51.5 25.6 927 4 US-10-369-493-6571 Sequence 6571, Ap  
260 51.5 25.6 999 4 US-10-369-493-5671 Sequence 5671, Ap  
261 51.5 25.6 999 4 US-10-369-493-5672 Sequence 5672, Ap  
262 51.5 25.6 1450 4 US-10-463-929-197 Sequence 197, App  
263 51.5 25.6 2052 4 US-10-437-963-137285 Sequence 137285,  
264 51 25.4 63 4 US-10-424-599-191209 Sequence 191209,  
265 51 25.4 70 4 US-10-380-703-23 Sequence 23, Appl  
266 51 25.4 70 4 US-10-380-703-26 Sequence 26, Appl  
267 51 25.4 70 4 US-10-380-703-30 Sequence 30, Appl  
268 51 25.4 70 6 US-11-021-874-156 Sequence 156, App  
269 51 25.4 70 6 US-11-021-874-159 Sequence 159, App  
270 51 25.4 70 6 US-11-021-874-163 Sequence 163, App  
271 51 25.4 78 3 US-09-749-637A-324 Sequence 324, App  
272 51 25.4 78 5 US-10-839-227-324 Sequence 324, App  
273 51 25.4 91 5 US-10-450-763-30480 Sequence 30480, A  
274 51 25.4 116 4 US-10-424-599-276838 Sequence 276838, A  
275 51 25.4 117 3 US-09-950-933A-62 Sequence 62, Appl  
276 51 25.4 117 4 US-10-424-599-191216 Sequence 191216,  
277 51 25.4 119 3 US-09-950-933A-63 Sequence 63, Appl  
278 51 25.4 125 4 US-10-437-963-136584 Sequence 136584,  
279 51 25.4 175 4 US-10-767-701-62745 Sequence 62745, A  
280 51 25.4 197 4 US-10-425-115-273823 Sequence 273823,  
281 51 25.4 197 4 US-10-425-115-302621 Sequence 302621,  
282 51 25.4 252 4 US-10-425-114-63189 Sequence 63189, A  
283 51 25.4 260 4 US-10-437-963-186621 Sequence 186621,  
284 51 25.4 308 4 US-10-425-115-249202 Sequence 249202,  
285 51 25.4 361 5 US-10-450-763-34909 Sequence 34909, A  
286 51 25.4 645 5 US-10-739-930-6375 Sequence 6375, Ap  
287 51 25.4 818 4 US-10-369-493-18031 Sequence 18031, A  
288 51 25.4 858 4 US-10-437-963-127781 Sequence 127781,  
289 51 25.4 1857 4 US-10-437-963-1522007 Sequence 152007,  
290 50.5 25.1 99 4 US-10-437-963-199882 Sequence 199882,  
291 50.5 25.1 119 4 US-10-767-701-55749 Sequence 55749, A  
292 50.5 25.1 139 4 US-10-437-963-152280 Sequence 152280,  
293 50.5 25.1 159 4 US-10-425-115-265606 Sequence 265606,  
294 50.5 25.1 182 4 US-10-424-599-213191 Sequence 213191,  
295 50.5 25.1 191 3 US-09-950-933A-66 Sequence 66, Appl  
296 50.5 25.1 191 4 US-10-424-599-213188 Sequence 213188,  
297 50.5 25.1 198 4 US-10-425-115-208386 Sequence 208386,  
298 50.5 25.1 435 4 US-10-237-790-10 Sequence 10, Appl  
299 50.5 25.1 541 4 US-10-425-114-72556 Sequence 72556, A  
300 50.5 25.1 575 3 US-09-796-753-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-854-864-7  
; Sequence 7, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-7  
  
Query Match 100.0%; Score 201; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CSQNEVFDLLHACIPQCLRCSSNTPLTCQRYC 34  
|||||  
DB 1 CSQNEVFDLLHACIPQCLRCSSNTPLTCQRYC 34  
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RESULT 2  
US-09-855-158-7  
; Sequence 7, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLI  
; TITLE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-7  
  
Query Match 100.0%; Score 201; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CSQNEVFDLLHACIPQCLRCSSNTPLTCQRYC 34  
|||||  
DB 1 CSQNEVFDLLHACIPQCLRCSSNTPLTCQRYC 34  
|||||  
  
RESULT 3  
US-09-854-864-6  
; Sequence 6, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match      100.0%; Score 201; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34
Db 5 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 38

RESULT 4
US-09-855-158-6
; Sequence 6, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

Query Match      100.0%; Score 201; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34
Db 5 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 38

RESULT 5
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      100.0%; Score 201; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34
Db 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 6
US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match      100.0%; Score 201; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34
Db 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 7
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      100.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34
Db 1 CSQNEFYDSSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 8
US-09-855-158-13
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; Sequence 13, Application US/09855158		; FILE REFERENCE: A-686A	
; Publication No. US20020086018A1		; CURRENT APPLICATION NUMBER: US/09/855,158	
; GENERAL INFORMATION:		; CURRENT FILING DATE: 2001-09-11	
; APPLICANT: THEILL, LARS EYDE		; PRIOR APPLICATION NUMBER: US 60/214,591	
; APPLICANT: YU, GANG		; PRIOR FILING DATE: 2000-06-27	
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BU		; PRIOR APPLICATION NUMBER: US 60/204,039	
; TITLE OF INVENTION: 3, AND TACI		; PRIOR FILING DATE: 2000-05-12	
; FILE REFERENCE: A-686A		; NUMBER OF SEQ ID NOS: 30	
; CURRENT APPLICATION NUMBER: US/09/855,158		; SOFTWARE: PatentIn version 3.1	
; CURRENT FILING DATE: 2001-09-11		; SEQ ID NO 5	
; PRIOR APPLICATION NUMBER: US 60/214,591		; LENGTH: 181	
; PRIOR FILING DATE: 2000-06-27		; TYPE: PRT	
; PRIOR APPLICATION NUMBER: US 60/204,039		; ORGANISM: Homo sapiens	
; PRIOR FILING DATE: 2000-05-12		US-09-855-158-5	
; NUMBER OF SEQ ID NOS: 30		Query Match	
; SOFTWARE: PatentIn version 3.1		Best Local Similarity	
; SEQ ID NO 13		Matches	
; LENGTH: 81		34; Conservative	
; TYPE: PRT		0; Mismatches	
; ORGANISM: Consensus		0; Indels	
US-09-855-158-13		0; Gaps	
		0; Length 81;	
Query Match		100.0%; Score 201; DB 3;	
Best Local Similarity		100.0%; Pred. No. 4.9e-17;	
Matches		34; Conservative	
0; Mismatches		0; Indels	
0; Gaps		0; Length 181;	
Qy		1 CSQNEYFDSLHACIPQQLRCSSTPPLTCQRYC 34	
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; Patent No. US20020081296A1		; GENERAL INFORMATION:	
; APPLICANT: THEILL, LARS EYDE		; APPLICANT: YU, GANG	
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,		; TITLE OF INVENTION: BLYS/AGP-3, AND TACI	
; FILE REFERENCE: A-686B		; CURRENT APPLICATION NUMBER: US/09/854,864	
; CURRENT FILING DATE: 2001-09-11		; CURRENT FILING DATE: 2001-09-11	
; PRIOR APPLICATION NUMBER: US 60/204,039		; PRIOR FILING DATE: 2000-05-12	
; PRIOR FILING DATE: 2000-06-27		; PRIOR APPLICATION NUMBER: US 60/214,591	
; NUMBER OF SEQ ID NOS: 31		; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 5		; LENGTH: 181	
; TYPE: PRT		; ORGANISM: Homo sapiens	
US-09-854-864-5		Query Match	
		Best Local Similarity	
		Matches	
		34; Conservative	
		0; Mismatches	
		0; Indels	
		0; Gaps	
		0; Length 181;	
Qy		1 CSQNEYFDSLHACIPQQLRCSSTPPLTCQRYC 34	
Db		5 CSQNEYFDSLHACIPQQLRCSSTPPLTCQRYC 38	
RESULT 10		US-09-855-158-5	
US-09-855-158-5		; Sequence 5, Application US/09855158	
; Publication No. US20020086018A1		; GENERAL INFORMATION:	
; APPLICANT: THEILL, LARS EYDE		; APPLICANT: YU, GANG	
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BU		; TITLE OF INVENTION: 3, AND TACI	

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; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 13
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 14
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 15
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

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RESULT 16
US-10-151-882-47
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 17
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; PRIOR FILING DATE: 2002-05-20
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 18
US-10-008-063-7
; Sequence 7, Application US/1008063
; Publication No. US2003092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TALE-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 19
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; PRIOR FILING DATE: 2002-05-20
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 20
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALE-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
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US-10-216-074-11

Query Match 100.0%; Score 201; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCORYC 34  
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Db 8 CSONEYFDSLHACIPQLRCSSNTPPLTCORYC 41

RESULT 21

US-10-087-080-39

; Sequence 39, Application US/10087080  
; Publication No. US2003235820A1  
; GENERAL INFORMATION:  
; APPLICANT: Mack, David H.  
; APPLICANT: Markowitz, Sanford David  
; APPLICANT: Eos Biotechnology, Inc.  
; APPLICANT: Case Western Reserve University  
; TITLE OF INVENTION: No. US2003235820A1el Methods of Diagnosis of Metastatic Colorectal Cancer  
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for  
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer  
; FILE REFERENCE: 018501-000840US  
; CURRENT APPLICATION NUMBER: US/10/087,080  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US 60/272,206  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: US 60/281,149  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/284,555  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member  
; OTHER INFORMATION: 17 (TNFRSF17)

US-10-087-080-39

Query Match 100.0%; Score 201; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCORYC 34  
| | | | | | | | | | | | | | | | | | | |  
Db 8 CSONEYFDSLHACIPQLRCSSNTPPLTCORYC 41

RESULT 22

US-10-742-634-9

; Sequence 9, Application US/10742634  
; Publication No. US20040208824A1  
; GENERAL INFORMATION:  
; APPLICANT: Parmelee, David  
; APPLICANT: Yen, Ren-Hwa  
; APPLICANT: Galperina, Olga  
; APPLICANT: Hilbert, David  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Thereof  
; FILE REFERENCE: 1488.1810002  
; CURRENT APPLICATION NUMBER: US/10/742,634  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: US 60/435,262  
; PRIOR FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 60/467,198  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9

```
Best Local Similarity 100.0%; Pred. No. 1.le-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34  
DB 8 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 41

```

RESULT 25
US-10-861-049-27
; Sequence 27, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: *Oian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-27

```

```

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34: Conservative 0; Mismatches 0; Indels

```

Qy	1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Dh	8 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 26  
US-10-989-826-46  
; Sequence 46, Application US/10989826  
; Publication No. US20050238650A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Crowley, Craig  
; APPLICANT: De Sauvage, Frederic J.  
; APPLICANT: Eaton, Daniel L.  
; APPLICANT: Ebens, Allen  
; APPLICANT: Polson, Andrew  
; APPLICANT: Smith, Victoria  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of  
; TITLE OF INVENTION: Hematopoietic Origin  
; FILE REFERENCE: P5105R1US  
; CURRENT APPLICATION NUMBER: US/10/989,826  
; CURRENT FILING DATE: 2004-11-16  
; PRIOR APPLICATION NUMBER: US 60/520,842  
; PRIOR FILING DATE: 2003-11-17  
; PRIOR APPLICATION NUMBER: US 60/532,426  
; PRIOR FILING DATE: 2003-12-24  
; NUMBER OF SEQ ID NOS: 75  
; SEQ ID NO 46  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-989-826-46

Query Match 100.0%; Score 201; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels

QY	1	CSQNEYFDSLLHACIPQLRCSNTPLTCQRYC	34
QY	1	CSQNEYFDSLLHACIPQLRCSNTPLTCQRYC	34
ph	8	CSQNEYFDSLLHACIPQLRCSNTPLTCQRYC	41

RESULT 27  
US-11-021-874-27  
Sequence 27, Application US/11021874  
Publication No. US20050163775A1  
GENERAL INFORMATION:  
APPLICANT: Andrew Chan  
APPLICANT: Qian Gong  
APPLICANT: Flavius Martin  
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
FILE REFERENCE: P2040R1P1  
CURRENT APPLICATION NUMBER: US/11/021.874  
CURRENT FILING DATE: 2004-12-22  
PRIORITY APPLICATION NUMBER: US 10/861,049  
PRIORITY FILING DATE: 2004-06-04  
PRIORITY APPLICATION NUMBER: US 60/476,531  
PRIORITY FILING DATE: 2003-06-06  
PRIORITY APPLICATION NUMBER: US 60/476,481  
PRIORITY FILING DATE: 2003-06-05  
PRIORITY APPLICATION NUMBER: US 60/476,414  
PRIORITY FILING DATE: 2003-06-05  
NUMBER OF SEQ ID NOS: 165  
SEQ ID NO 27  
LENGTH: 184  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-021-874-27

Query Match	100.0%;	Score 201;	DB 6;	Length 184;
Best Local Similarity	100.0%;	Pred. No. 1.1e-16;		
Matches 34:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

QY	1 CSONEYFDSLLHACIPCOLRCSSNTPLTCQRYC 34
pB	8 CSONEYFDSLLHACIPCOLRCSSNTPLTCQRYC 41

RESULT 28  
US-09-854-864-9  
; Sequence 9, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION: LARS EYDE  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-9

Query Match	100.0%;	Score 201;	DB 3;	Length 283;
Best Local Similarity	100.0%;	Pred. No. 1.6e-16;		
Matches 34.	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

**Oy** 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 34  
| | | | | | | | | | | | | | | | | | | | |  
**nb** 5 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 38  
| | | | | | | | | | | | | | | | | | | | |

```

RESULT 29
US-09-855-158-9
; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BU
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match      100.0%; Score 201; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 38

RESULT 30
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match      100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 31 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 64

RESULT 31
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match      90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.3e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 46 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 99

RESULT 32
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match      90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.3e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 46 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 99
```

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Qy      1  CSONEYFDSL-----LHACIPQCLRCSSNTPELTCQRYC 33
      |||||||
Db      46  CSONEYFDSLHACIPQCLRCSSNTPPLTCLHACIPQCLRCSSNTPELTCQRYC 99

RESULT 33
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING AP
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

```

```

; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-074-17

Query Match          67.7%; Score 136; DB 4; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.5e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
      :|||||:|||||:|||||:|||||:|||||
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 36
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match          67.7%; Score 136; DB 3; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
      :|||||:|||||:|||||:|||||:|||||
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 37
US-09-855-158-10
; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

```

```
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match
Best Local Similarity 67.7%; Score 136; DB 3; Length 281;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSONEYFDSLHACIPCQLRCSNTPTLCQRYC 34
|:|||||||||:|||||:|||||
Db 5 CFHSEYFDSLHACKCHLRCSN--PPATCQPYC 36
|:|||||||||:|||||:|||||

RESULT 38
US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZHONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match
Best Local Similarity 61.7%; Score 124; DB 4; Length 42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCQLRC 21
|:|||||||||:|||||
Db 22 CSONEYFDSLHACIPCQLRC 42
|:|||||||||:|||||

RESULT 39
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match
Best Local Similarity 46.5%; Score 93.5; DB 3; Length 117;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLHACIPCQLRCSNTPTLCQRYC 34
|:|||||||||:|||||:|||||
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27
|:|||||||||:|||||:|||||

RESULT 40
US-09-855-158-12
; Sequence 12, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-855-158-12

Query Match
Best Local Similarity 46.5%; Score 93.5; DB 3; Length 117;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLHACIPCQLRCSNTPTLCQRYC 34
|:|||||||||:|||||:|||||
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27
|:|||||||||:|||||:|||||

RESULT 41
US-10-087-192-1647
; Sequence 1647, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1647
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1647
```



Query Match 35.6%; Score 71.5; DB 4; Length 249;  
Best Local Similarity 35.3%; Pred. No. 0.97;  
Matches 12: Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy	1	CSQNEYFDSLHACIPQLRCCSSNTPLTCQRVC	34
		: :   :   :   :   :   :   :	
Db	6	CPKDOYDSSRKSCVSCALTCQSORS-QRTCTDFC	38

```

RESULT 42
US-10-180-903-2
; Sequence 2, Application US/10180903
; Publication No. US20030093824A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; THEREO
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; PRIORITY FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIORITY FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIORITY FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-10-180-903-2

```

```

RESULT 43
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779, 050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181, 800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-45

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QY	1	CSONEYFDSILHACIPQLRCSSNTPLTCQRYC	34
		: :   :   :   :   :   :   :   :	
n6	2	CPREYWDPIIGTQMSCKTICNHOS-RTCAAF	34

RESULT 44  
US-09-854-864-20

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; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; OS-09-854-864-20

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**QY** 1 CSQNEYPDSLHACIPQLRCSNTPPLTCQRVC 34  
| : : | | | : : | : : | : :

**Dd** 1 CPREOYWDPLLGTGCMCKTICNHOS-QRTCAAF 33

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RESULT 45
US-09-855-158-20
; Sequence 20, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: 3, AND TAC1
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-20

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**QY** 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRVC 34  
| : : | | : : | : : | : : |  
**nB** 1 CPPEOYWDPLLGTMCMSKTCICNHOS-QRTCAAF 33

RESULT 46  
US-03-854-864-16  
; Sequence 16, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COM  
; TITLE OF INVENTION: BLYS/AGP-3, AN







```

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-376-2

Query Match 33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPELTQRYC 34
| : : | | | : : : : : : : : : :
Db 34 CPBEQYWDPLLGTCSCKTICNHQS-ORTCAAF 66

RESULT 62
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-42

Query Match 33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPQCLRCSSNTPELTQRYC 34
| : : | | | : : : : : : : : : :
Db 34 CPBEQYWDPLLGTCSCKTICNHQS-ORTCAAF 66

RESULT 63
US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wawan S
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

```



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; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 66

RESULT 69
US-10-293-816-2
; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 66

RESULT 70
US-10-008-063-8
; Sequence 8, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-8

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 66

RESULT 71
US-10-152-363A-2
; Sequence 2, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 66

RESULT 72
US-10-268-951-22
; Sequence 22, Application US/10268951
; Publication No. US2003016864A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTQCRYC 34
Db      34 CPEEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 73
US-10-258-368-1
; Sequence 1, Application US/10258368
; Publication No. US20040013674A1
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTQCRYC 34
Db      34 CPEEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 74
US-10-618-797-4
; Sequence 4, Application US/10618797
; Publication No. US20040048296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon
; FILE REFERENCE: PF527D1
; CURRENT APPLICATION NUMBER: US/10/618,797
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 09/848, 295
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
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; ORGANISM: human
US-10-618-797-4

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTQCRYC 34
Db      34 CPEEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

RESULT 75
US-10-742-634-7
; Sequence 7, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Thereof
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTQCRYC 34
Db      34 CPEEQYWDPLLGTGCMCKTICNHQS-QRTCAAF 66

Search completed: December 21, 2005, 16:30:38
Job time : 90.4 secs
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247	49	24.4	3635	2	US-10-037-417-47	Sequence 47, Appl
248	49	24.4	3635	2	US-10-037-182-4	Sequence 4, Appl
249	48.5	24.1	348	2	US-10-188-495-69	Sequence 69, Appl
250	48.5	24.1	590	1	US-08-448-196A-9	Sequence 9, Appl
251	48	23.9	56	1	US-08-358-160-151	Sequence 151, App
252	48	23.9	95	2	US-09-177-249-273	Sequence 273, App
253	48	23.9	95	2	US-09-812-283-273	Sequence 273, App
254	48	23.9	99	2	US-09-950-933A-64	Sequence 64, Appl
255	48	23.9	116	2	US-09-270-767-39208	Sequence 39208, A
256	48	23.9	116	2	US-09-270-767-54425	Sequence 54425, A
257	48	23.9	127	2	US-09-489-039A-11660	Sequence 11660, A
258	48	23.9	276	2	US-09-270-767-32903	Sequence 32903, A
259	48	23.9	276	2	US-09-270-767-48120	Sequence 48120, A
260	48	23.9	448	2	US-09-342-681C-17	Sequence 17, Appl
261	48	23.9	448	2	US-09-342-681C-19	Sequence 19, Appl
262	48	23.9	500	1	US-08-896-005-1	Sequence 1, Appl
263	48	23.9	689	2	US-09-177-249-2	Sequence 2, Appl
264	48	23.9	689	2	US-09-061-769A-2	Sequence 2, Appl
265	48	23.9	689	2	US-09-812-283-2	Sequence 2, Appl
266	48	23.9	689	2	US-10-176-884-14	Sequence 14, Appl
267	48	23.9	784	2	US-09-949-016-9367	Sequence 9367, Ap
268	48	23.9	932	2	US-10-176-884-15	Sequence 15, Appl
269	48	23.9	969	1	US-08-284-941-2	Sequence 2, Appl
270	48	23.9	969	1	US-08-447-642-2	Sequence 2, Appl
271	48	23.9	969	2	US-09-236-503-2	Sequence 6, Appl
272	48	23.9	969	2	US-09-361-403-6	Sequence 6, Appl
273	48	23.9	969	2	US-09-949-016-6240	Sequence 6240, Ap
274	48	23.9	969	4	PCT-US93-02147A-2	Sequence 2, Appl
275	47.5	23.6	122	2	US-09-513-999C-7856	Sequence 7856, Ap
276	47.5	23.6	197	2	US-09-370-838-206	Sequence 206, App
277	47.5	23.6	197	2	US-09-854-133-206	Sequence 206, App
278	47.5	23.6	865	2	US-09-902-540-10416	Sequence 10416, A
279	47.5	23.6	1798	2	US-09-845-583A-8	Sequence 8, Appl
280	47.5	23.6	1798	2	US-09-561-709B-11	Sequence 11, Appl
281	47.5	23.6	1798	2	US-09-917-254-87	Sequence 87, Appl
282	47.5	23.6	1854	2	US-09-949-016-11625	Sequence 11625, A
283	47.5	23.6	3597	2	US-10-037-417-6	Sequence 6, Appl
284	47.5	23.6	3600	2	US-10-037-417-2	Sequence 2, Appl
285	47	23.4	127	2	US-10-104-047-3105	Sequence 3105, Ap
286	47	23.4	134	2	US-09-830-230A-676	Sequence 676, App
287	47	23.4	137	2	US-09-328-352-5960	Sequence 5960, Ap
288	47	23.4	172	2	US-09-830-230A-675	Sequence 675, App
289	47	23.4	209	2	US-09-270-767-41054	Sequence 41054, A
290	47	23.4	209	2	US-09-270-767-56270	Sequence 56270, A
291	47	23.4	293	2	US-09-902-540-16212	Sequence 16212, A
292	47	23.4	339	2	US-09-686-583B-40	Sequence 40, Appl
293	47	23.4	349	2	US-09-006-353A-13	Sequence 13, Appl
294	47	23.4	349	2	US-09-573-986-13	Sequence 13, Appl
295	47	23.4	381	2	US-09-686-583B-48	Sequence 48, Appl
296	47	23.4	397	2	US-09-686-583B-43	Sequence 43, Appl
297	47	23.4	478	2	US-09-004-838-105	Sequence 105, App
298	47	23.4	480	2	US-09-004-838-49	Sequence 49, Appl
299	47	23.4	481	2	US-09-902-540-13111	Sequence 13111, A
300	47	23.4	609	1	US-08-716-301-4	Sequence 4, Appl

RESULT 1

US-09-854-864-7

Prior Application Number: US/09854864

Sequence 7, Application US/09854864

Patent No. 6774106

General Information:

Applicant: THEILL, LARS EYDE

Applicant: YU, GANG

Title of Invention: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

Title of Invention: BLYS/AGP-3, AND TACI

File Reference: A-686B

Current Application Number: US/09/854,864

Prior Filing Date: 2001-09-11

Prior Application Number: US 60/204,039

Prior Filing Date: 2000-05-12

Query Match

Best Local Similarity 100.0%; Score 201; DB 2; Length 51;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CSQNEVFDLSLLHACIPQCLRCSSNTPTPLTCQRYC 34

|||||

DB

1 CSQNEVFDLSLLHACIPQCLRCSSNTPTPLTCQRYC 34

|||||

RESULT 2

US-09-854-864-6

Prior Application Number: US/09854864

Sequence 6, Application US/09854864

Patent No. 6774106

General Information:

Applicant: THEILL, LARS EYDE

Applicant: YU, GANG

Title of Invention: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

Title of Invention: BLYS/AGP-3, AND TACI

File Reference: A-686B

Current Application Number: US/09/854,864

Prior Filing Date: 2001-09-11

Prior Application Number: US 60/204,039

Prior Filing Date: 2000-05-12

Query Match

Best Local Similarity 100.0%; Score 201; DB 2; Length 51;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CSQNEVFDLSLLHACIPQCLRCSSNTPTPLTCQRYC 34

|||||

DB

5 CSQNEVFDLSLLHACIPQCLRCSSNTPTPLTCQRYC 38

|||||

RESULT 3

US-09-854-864-21

Prior Application Number: US/09854864

Sequence 21, Application US/09854864

Patent No. 6774106

General Information:

Applicant: THEILL, LARS EYDE

Applicant: YU, GANG

Title of Invention: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

Title of Invention: BLYS/AGP-3, AND TACI

File Reference: A-686B

Current Application Number: US/09/854,864

Prior Filing Date: 2001-09-11

Prior Application Number: US 60/204,039

Prior Filing Date: 2000-05-12

Query Match

Best Local Similarity 100.0%; Score 201; DB 2; Length 51;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CSQNEVFDLSLLHACIPQCLRCSSNTPTPLTCQRYC 34

|||||

DB

5 CSQNEVFDLSLLHACIPQCLRCSSNTPTPLTCQRYC 38

|||||

ALIGNMENTS

US-09-854-864-7

Prior Application Number: US/09854864

Sequence 7, Application US/09854864

Patent No. 6774106

General Information:

Applicant: THEILL, LARS EYDE

Applicant: YU, GANG

Title of Invention: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

Title of Invention: BLYS/AGP-3, AND TACI

File Reference: A-686B

Current Application Number: US/09/854,864

Prior Filing Date: 2001-09-11

Prior Application Number: US 60/204,039

Prior Filing Date: 2000-05-12

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; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      100.0%; Score 201; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34

RESULT 4
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-04-039
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      100.0%; Score 201; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34

RESULT 5
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-04-039
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      100.0%; Score 201; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 49

RESULT 6
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 41

RESULT 7
US-09-949-016-11115
; Sequence 1115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11115
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11115

Query Match      100.0%; Score 201; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 34
Db 16 CSQNEYFDSLHACIPCOLRCSNTTPTLCQRYC 49

RESULT 8
US-09-854-864-9
```



```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match          33.1%; Score 66.5; DB 2; Length 117;
Best Local Similarity 32.4%; Pred. No. 0.00052;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
   :|||:|||||:|||||:|||||:|||||:
Db 2 AQCEYWDPLLGTCMSCKTICNHQS-QRTCAAF 27

RESULT 13
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match          33.1%; Score 66.5; DB 2; Length 59;
Best Local Similarity 32.4%; Pred. No. 0.42;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
   :|||:|||||:|||||:|||||:|||||:
Db 1 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 33

RESULT 14
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match          33.1%; Score 66.5; DB 2; Length 166;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
   :|||:|||||:|||||:|||||:|||||:
Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 66

RESULT 16
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
```



```
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-810-572A-2

Query Match 33.1%; Score 66.5; DB 1; Length 293;
Best Local Similarity 32.4%; Pred. No. 2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTQRYC 34
Db 34 CPEQYWDPLGTGTCMCKTICNHQS-QRTCAAF 66

RESULT 20
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 33.1%; Score 66.5; DB 2; Length 293;
Best Local Similarity 32.4%; Pred. No. 2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTQRYC 34
Db 34 CPEQYWDPLGTGTCMCKTICNHQS-QRTCAAF 66

RESULT 21
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 33.1%; Score 66.5; DB 2; Length 293;
Best Local Similarity 32.4%; Pred. No. 2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTQRYC 34
Db 34 CPEQYWDPLGTGTCMCKTICNHQS-QRTCAAF 66

RESULT 21
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
```



```

, NAME: Jackson Esq., David A.
, REGISTRATION NUMBER: 26,742
, REFERENCE/DOCKET NUMBER: 1340-1-007
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 201-487-5800
, TELEFAX: 201-343-1684
, INFORMATION FOR SEQ ID NO: 2:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 293 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, HYPOTHETICAL: NO
, FRAGMENT TYPE: N-terminal
, ORIGINAL SOURCE:
, ORGANISM: Homo sapiens
, SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

```

Query Match	33.1%;	Score 66.5;	DB 2;	Length 293;
Best Local Similarity	32.4%;	Pred. No. 2;		
Matches 11: Conservative	8;	Mismatches 14;	Indels 1;	Gaps 1;

**Qy**            1 CSQNEYFDLLHACIPQLRCSSNTPPLTCQRVC 34  
| : | : | : | : | : | :  
**Dd**            34 CPREEYWDPLLGTGMSCKTINHQS-ORTCAAFc 66

RESULT 22

```

US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

```

Query Match	33.1%;	Score 66.5;	DB 2;	Length 293;
Best Local Similarity	32.4%;	Pred. No. 2;		
Matches	11;	Conservative	8;	Mismatches 14;
				Indels 1;
				Gaps 1;

**QY**            1 CSONEYFDSLILHACIPQLRCSSNTPLTCQRVC 34  
       | : : : | | | : : : | : : | : : |  
**Db**            34 CPREOYWDPLLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 23

```

US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; TITLE OF INVENTION: Thereon
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-848-295-4

```

Query Match 33.1%; Score 66.5; DB 2; Length 293;  
Best Local Similarity 32.4%; Pred. No. 2;  
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

**Qy**            1 CSQNEYFDLSLLHACIPQLRCSSNTPLTTCQRYC 34  
| : : | | | : : | : : | : :  
**Dp**            34 CPKEEYDPLLLGTMCCKITCNHQ-SORTCAAF 66

RESULT 24

US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: prt  
; ORGANISM: Homo sapiens  
US-09-854-864-14

Query Match	33.1%;	Score 66.5;	DB 2;	Length 293;
Best Local Similarity	32.4%;	Pred. No. 2;		
Matches 11: Conservative		8;	Mismatches 14;	Indels 1;
				Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRVC 34  
| : | : | : | : | : | : | : | :  
pb 34 CPREEYDPLLGTCWMSCKTICNHOS-ORTCAAFc 66

RESULT 25

```

US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B

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```
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-18

Query Match          33.1%; Score 66.5; DB 2; Length 397;
Best Local Similarity 32.4%; Pred. No. 2.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPPLTCORVC 34
Db 34 CPBEQYDPLLTGCMCKTICNHQS-ORTCAAPC 66

RESULT 26
US-09-949-016-9626
; Sequence 9626, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9626
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9626

Query Match          30.3%; Score 61; DB 2; Length 1106;
Best Local Similarity 28.0%; Pred. No. 32;
Matches 14; Conservative 6; Mismatches 14; Indels 16; Gaps 2;

QY 1 CSQNEYFDSLHACIPCOLRC-----SSTPPL-----TCORVC 34
Db 899 CSFSEYDEDAPEGCKKCHVKCFHGMGPAEDQCQTCPMNSLLLTTCVKDC 948

RESULT 27
US-10-104-047-2804
; Sequence 2804, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2804
; LENGTH: 581
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2804

Query Match          29.6%; Score 59.5; DB 2; Length 581;
Best Local Similarity 28.9%; Pred. No. 26;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOL-----RCSNNT 25
Db 337 CSPGHYYNTSIHRCIRCAMGYSQPDFRQNFCSRCPGNT 374

RESULT 28
US-10-104-047-2834
; Sequence 2834, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2834
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2834

Query Match          29.6%; Score 59.5; DB 2; Length 880;
Best Local Similarity 28.9%; Pred. No. 39;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOL-----RCSNNT 25
Db 636 CSPGHYYNTSIHRCIRCAMGYSQPDFRQNFCSRCPGNT 673

RESULT 29
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF INVENTIONS: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,967
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-967-2

Query Match      27.9%; Score 56; DB 1; Length 2476;
Best Local Similarity 31.6%; Pred. No. 2.7e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSQNEYFDSLHACIP-CQ---LRCSSTNPPLTCQRYC 34
Db 1851 CSAHSVYTCVPSCLPSCQDEGQCTGAGAPSTCEGCG 1888

RESULT 30
US-09-621-976-6330
; Sequence 6330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6330
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6330

Query Match      26.9%; Score 54; DB 2; Length 98;
Best Local Similarity 38.1%; Pred. No. 21;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 14 CIPCOLRCSSNTPLTCQRYC 34
Db 58 CLPCFSQSPSCPPQPCTKPC 78

RESULT 31
US-09-471-276-1590
; Sequence 1590, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: FCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1590
; LENGTH: 98
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1590

Query Match      26.9%; Score 54; DB 2; Length 98;
Best Local Similarity 38.1%; Pred. No. 21;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 14 CIPCOLRCSSNTPLTCQRYC 34
Db 58 CLPCFSQSPSCPPQPCTKPC 78

RESULT 32
US-09-252-991A-25721
; Sequence 25721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25721
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25721

Query Match      26.9%; Score 54; DB 2; Length 431;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 13 ACIPCOLRCSSNTPLTCQRYC 32
Db 242 AC--CRARCSNAPPTACRR 259

RESULT 33
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
US-09-257-580-2

Query Match      26.6%; Score 53.5; DB 2; Length 381;
Best Local Similarity 48.3%; Pred. No. 89;
Matches 14; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

QY 4 NEYFDSLHACIPCOLRCSSNTPLTCQRYC 32
Db 118 NKLFQCLAKTC-PVQLWVSSPPPTNCTVR 145
```

RESULT 34  
US-08-718-388-9  
; Sequence 9, Application US/08718388  
; Patent No. 6271362  
; GENERAL INFORMATION:  
; APPLICANT: MORIKAWA, MINORU  
; APPLICANT: HARADA, NAOKI  
; TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,388  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 0230-111  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5405 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-718-388-9

Query Match 26.6%; Score 53.5; DB 2; Length 5405;  
Best Local Similarity 34.3%; Pred. No. 1.2e+03;  
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEYFDSLHACI-PCQLRCSNTPTPLTCQRYC 34  
| | | : : : | | | : : : | | | : : : | | | : : : |  
Db 2733 CPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 2763

RESULT 35  
US-09-950-933A-61  
; Sequence 61, Application US/09950933A  
; Patent No. 6875907  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Navarro, Pedro  
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: 35718/238472  
; CURRENT APPLICATION NUMBER: US/09/950,933A  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/232,569  
; PRIOR FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-950-933A-61

Query Match 26.4%; Score 53; DB 2; Length 108;

Best Local Similarity 44.4%; Pred. No. 30;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 17 COLRCSNTPTPLTCQRYC 34  
| : | | : : : | | | : : : | | | : : : | | | : : : |  
Db 53 CKTRCSAHSRPNVCNRC 70

RESULT 36  
US-09-848-295-2  
; Sequence 2, Application US/09848295  
; Patent No. 6623941  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based  
; TITLE OF INVENTION: Thereon  
; FILE REFERENCE: PF527  
; CURRENT APPLICATION NUMBER: US/09/848,295  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/202,193  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-295-2

Query Match 26.1%; Score 52.5; DB 2; Length 142;  
Best Local Similarity 29.4%; Pred. No. 45;  
Matches 10; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPTPLTCQRYC 34  
| : | : | : | : | : | : | : | : | : | : | : | : |  
Db 4 CPEEQYMAALLGTCMFCFAICNHQS-QRTCAASC 36

RESULT 37  
US-09-950-933A-65  
; Sequence 65, Application US/09950933A  
; Patent No. 6875907  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Navarro, Pedro  
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: 35718/238472  
; CURRENT APPLICATION NUMBER: US/09/950,933A  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/232,569  
; PRIOR FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-950-933A-65

Query Match 25.9%; Score 52; DB 2; Length 115;  
Best Local Similarity 44.4%; Pred. No. 42;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 17 COLRCSNTPTPLTCQRYC 34  
| : | | : : : | | | : : : | | | : : : | | | : : : |  
Db 60 CTVRCSLHSPKICSRAC 77

RESULT 38  
US-09-877-730-26  
; Sequence 26, Application US/09877730



```
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-6

Query Match      25.9%; Score 52; DB 2; Length 904;
Best Local Similarity 33.3%; Pred. No. 3.1e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY      4 NEYFDSLLHACIPCOLRCSSNTPTPLTCQRY 33
      | : | : | : | : | : | : | : | : | : |
Db      860 NSPIDAKVLSCGICISRSISIPPCVCCKMY 889

RESULT 43
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 991
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12

Query Match      25.9%; Score 52; DB 2; Length 991;
Best Local Similarity 33.3%; Pred. No. 3.4e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY      4 NEYFDSLLHACIPCOLRCSSNTPTPLTCQRY 33
      | : | : | : | : | : | : | : | : | : |
Db      947 NSPIDAKVLSCGICISRSISIPPCVCCKMY 976

RESULT 44
US-09-877-730-2
; Sequence 2, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
```

```
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2

Query Match      25.9%; Score 52; DB 2; Length 1069;
Best Local Similarity 33.3%; Pred. No. 3.6e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY      4 NEYFDSLLHACIPCOLRCSSNTPTPLTCQRY 33
      | : | : | : | : | : | : | : | : | : |
Db      1025 NSPIDAKVLSCGICISRSISIPPCVCCKMY 1054

RESULT 45
US-08-117-080-12
; Sequence 12, Application US/08117080
; Patent No. 5482928
; GENERAL INFORMATION:
; APPLICANT: DE BOLLE, MIGUEL
; APPLICANT: BROEKAERT, WILLEM F
; APPLICANT: CAMMUE, BRUNO PA
; APPLICANT: VANDERLEYDEN, JOZEF
; APPLICANT: REES, SARAH B
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
; STREET: TOWER
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,080
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00423
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9105052.6
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9105684.6
; FILING DATE: 19-MAR-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861 3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
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ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2  
US-08-117-080-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;  
Best Local Similarity 38.5%; Pred. No. 27;  
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSNT-PPLTCQRYC 34  
Db 24 MIEACIGNGRCNENVPYCCSGFC 49

RESULT 46

US-08-471-329-12  
; Sequence 12, Application US/08471329  
; Patent No. 5689048  
; GENERAL INFORMATION:  
; APPLICANT: DE BOLLE, MIGUEL  
; APPLICANT: BROEKAERT, WILLEM F  
; APPLICANT: CAMMUE, BRUNO PA  
; APPLICANT: VANDERLEYDEN, JOZEF  
; APPLICANT: REES, SARAH B  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARB & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST  
; STREET: TOWER  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471.329  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117,080  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9105052.6  
; FILING DATE: 11-MAR-1991  
; APPLICATION NUMBER: US 08/117,080  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9105052.6  
; FILING DATE: 11-MAR-1991  
; APPLICATION NUMBER: GB 9105684.6  
; FILING DATE: 19-MAR-1991  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; TELEPHONE: (202) 861 3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2  
US-08-471-329-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;  
Best Local Similarity 38.5%; Pred. No. 27;  
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSNT-PPLTCQRYC 34  
Db 24 MIEACIGNGRCNENVPYCCSGFC 49

Db 24 MIEACIGNGRCNENVPYCCSGFC 49

RESULT 47

US-08-915-142-12  
; Sequence 12, Application US/08915142  
; Patent No. 5942663  
; GENERAL INFORMATION:  
; APPLICANT: DE BOLLE, MIGUEL  
; APPLICANT: BROEKAERT, WILLEM F  
; APPLICANT: CAMMUE, BRUNO PA  
; APPLICANT: VANDERLEYDEN, JOZEF  
; APPLICANT: REES, SARAH B  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARB & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST  
; STREET: TOWER  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915.142  
; FILING DATE: 20-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,329  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 08/117,080  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9105052.6  
; FILING DATE: 11-MAR-1991  
; APPLICATION NUMBER: GB 9105684.6  
; FILING DATE: 19-MAR-1991  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; TELEPHONE: (202) 861 3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2  
US-08-915-142-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;  
Best Local Similarity 38.5%; Pred. No. 27;  
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSNT-PPLTCQRYC 34  
Db 24 MIEACIGNGRCNENVPYCCSGFC 49

RESULT 48

US-08-465-380-4  
; Sequence 4, Application US/08465380  
; Patent No. 5863894

```
;
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-465-380-4

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
|:::| | | | | | | | | | | | | | | | | |
Db 6 CGENEWLDD---CGTQKPCAKCNEEPPEEDPICRSRC 42

RESULT 49
US-08-465-380-40
; Sequence 40, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
```

```
;
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-465-380-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
|:::| | | | | | | | | | | | | | | | | |
Db 6 CGENEWLDD---CGTQKPCAKCNEEPPEEDPICRSRC 42

RESULT 50
US-08-480-478-33
; Sequence 33, Application US/08480478
; Patent No. 5864009
; GENERAL INFORMATION:
; APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
; APPLICANT: HUGO STANSSENS; JORIS HILDA
; APPLICANT: LIEVEN MESSENS; MARC JOZEF
; APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
; APPLICANT: LAURENT STEPHANE JESPERS; and
; APPLICANT: YANNICK GEORGES JOZEF
; APPLICANT: GANSEMAN
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
; TITLE OF INVENTION: COAGULANT PROTEIN
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
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STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,965  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 210/243  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum

US-08-461-965-4

Query Match            25.6%; Score 51.5; DB 1; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY         1 CSONEYFDLSLHAC---IPQLRCSNTP----PLTCQRVC 34  
            |::|::|::|::|::|::|::|::|::|::|::|::|::|  
DDB         6 CGGENWLDD---CGTQKPCAKCNPEEPEDPICRSRG 42

RESULT 56  
US-08-461-965-40  
Sequence 40, Application US/08461965  
Patent No. 5872098

GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
FORM AND APPLICATION DATA:



TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-08-634-641-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34  
Db 6 CGENWLDD---CGTQKPCAKCNEPPPEEDPICSRGCC 42

RESULT 60

US-09-249-471-4

; Sequence 4, Application US/09249471

; Patent No. 6040441

; GENERAL INFORMATION:

; APPLICANT: Vlasuk, George Phillip

; APPLICANT: Stanssens, Patrick Eric Hugo

; APPLICANT: Messens, Joris Hilda Lieven

; APPLICANT: Lauwerys, Marc Josef

; APPLICANT: Laroche, Yves Rene

; APPLICANT: Jespers, Laurent Stephane

; APPLICANT: Gansemans, Yannick Georges Jozef

; APPLICANT: Moyle, Matthew

; APPLICANT: Beigum, Peter W.

; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

; NUMBER OF SEQUENCES: 356

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/249,471

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/809,455

; FILING DATE: April 17, 1997

; APPLICATION NUMBER: PCT/US95/13231

; FILING DATE: October 17, 1995

; APPLICATION NUMBER: 08/486,399

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/486,397

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/465,380

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/461,965

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/326,110

; FILING DATE: October 18, 1994

; ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 77 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

US-09-249-471-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;

Best Local Similarity 29.3%; Pred. No. 33;

Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34  
Db 6 CGENWLDD---CGTQKPCAKCNEPPPEEDPICSRGCC 42

RESULT 61

US-09-249-471-40

; Sequence 40, Application US/09249471

; Patent No. 6040441

; GENERAL INFORMATION:

; APPLICANT: Vlasuk, George Phillip

; APPLICANT: Stanssens, Patrick Eric Hugo

; APPLICANT: Messens, Joris Hilda Lieven

; APPLICANT: Lauwerys, Marc Josef

; APPLICANT: Laroche, Yves Rene

; APPLICANT: Jespers, Laurent Stephane

; APPLICANT: Gansemans, Yannick Georges Jozef

; APPLICANT: Moyle, Matthew

; APPLICANT: Beigum, Peter W.

; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

; NUMBER OF SEQUENCES: 356

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/249,471

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/809,455

; FILING DATE: April 17, 1997

; APPLICATION NUMBER: PCT/US95/13231

; FILING DATE: October 17, 1995

; APPLICATION NUMBER: 08/486,399

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/486,397

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/465,380

; FILING DATE: June 5, 1995

; APPLICATION NUMBER: 08/461,965

```
;
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-471-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSQNEVFDLSLLHAC---IPCQLRCSNTP-----PLTCORYC 34
Db 6 CGENEWLDLDD---CGTQKPCAEKCNPEEPEDPICRSRGC 42

RESULT 62
US-09-249-472-4
; Sequence 4, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansmans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,472
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
```

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;
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-472-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSQNEVFDLSLLHAC---IPCQLRCSNTP-----PLTCORYC 34
Db 6 CGENEWLDLDD---CGTQKPCAEKCNPEEPEDPICRSRGC 42

RESULT 63
US-09-249-472-40
; Sequence 40, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansmans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,472
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
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;; FILING DATE: October 17, 1995  
;; APPLICATION NUMBER: 08/486,399  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/486,397  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/465,380  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/461,965  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 216/270  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 40:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 77 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: Ancylostoma caninum  
;; US-09-249-472-40  
  
Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;  
  
Qy 1 CSQNEYFDSLHAC---IPQLRCSSNTP----PLTCORYC 34  
Db 6 CGENEWLLDD---CGTQKPCAKNRPPEEDPICRSRG 42  
  
RESULT 64  
US-09-249-451-4  
; Sequence 4, Application US/09249451  
; Patent No. 6087487  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Gansemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Peter W.  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,451  
; FILING DATE:

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/809,455  
;; FILING DATE: April 17, 1997  
;; APPLICATION NUMBER: PCT/US95/13231  
;; FILING DATE: October 17, 1995  
;; APPLICATION NUMBER: 08/486,399  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/486,397  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/465,380  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/461,965  
;; FILING DATE: June 5, 1995  
;; APPLICATION NUMBER: 08/326,110  
;; FILING DATE: October 18, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIGGS, SUZANNE L.  
;; REGISTRATION NUMBER: 30,158  
;; REFERENCE/DOCKET NUMBER: 216/270  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 77 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: Ancylostoma caninum  
;; US-09-249-451-4  
  
Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;  
  
Qy 1 CSQNEYFDSLHAC---IPQLRCSSNTP----PLTCORYC 34  
Db 6 CGENEWLLDD---CGTQKPCAKNRPPEEDPICRSRG 42  
  
RESULT 65  
US-09-249-451-40  
; Sequence 40, Application US/09249451  
; Patent No. 6087487  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Lieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Gansemans, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,451  
; FILING DATE:





ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,455  
FILING DATE: April 17, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-08-809-455-40  
  
Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;  
  
Qy 1 CSQNEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34  
Db 6 CGENEWLLD-----CGTQKPCAKCNBPPPEEDPICRSRG 42  
  
RESULT 68  
US-09-249-461-4  
Sequence 4, Application US/09249461  
Patent No. 6096877  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Larocche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Gangsemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Berghum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,461  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-09-249-461-4  
  
Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;  
  
Qy 1 CSQNEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34  
Db 6 CGENEWLLD-----CGTQKPCAKCNBPPPEEDPICRSRG 42  
  
RESULT 69  
US-09-249-461-40  
Sequence 40, Application US/09249461  
Patent No. 6096877  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Larocche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Gangsemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Berghum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: US/09/249,461  
PRIOR APPLICATION DATA:  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: 08/809,455  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-09-249-461-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP-----PLTCQRYC 34  
Db 6 CGENEWDD---CGTQKPCAKCNPEEPEDPICRSRGC 42

## RESULT 70

US-09-249-448-4  
Sequence 4, Application US/09249448  
Patent No. 6121435  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Gansmans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Berghum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: US/09/249,448  
PRIOR APPLICATION DATA:  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: 08/809,455  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-09-249-448-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP-----PLTCQRYC 34  
Db 6 CGENEWDD---CGTQKPCAKCNPEEPEDPICRSRGC 42

## RESULT 71

US-09-249-448-40  
Sequence 40, Application US/09249448  
Patent No. 6121435  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane

```

;
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Beigum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,448
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-448-40
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; Query Match 25.6%; Score 51.5; DB 2; Length 77;
; Best Local Similarity 29.3%; Pred. No. 33;
; Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
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; QY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP-----PLTCORYC 34
; 6 CGENEWLDD---CGTQKPCCEAKNCNEPPEEDPICRSRG 42
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; Db
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; RESULT 72
; US-09-249-473-4
; Sequence 4, Application US/09249473
; Patent No. 6534629
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
;
; APPLICANT: Messens, Joris Hilda Lieve
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Beigum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,473
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-473-4
;
; Query Match 25.6%; Score 51.5; DB 2; Length 77;
; Best Local Similarity 29.3%; Pred. No. 33;
; Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;
;
; QY 1 CSQNEYFDSLHAC---IPCQLRCSSNTP-----PLTCORYC 34
; 6 CGENEWLDD---CGTQKPCCEAKNCNEPPEEDPICRSRG 42
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; Db
;
; RESULT 73
; US-09-249-473-40
; Sequence 40, Application US/09249473
;

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US-09-498-556-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHLHAC---IPCQLRCSSTNP-----PLTCORYC 34  
DB 6 CGENEWLDD---CGTQKPCCAKCNPEEPPEEDPICRSRGC 42

Search completed: December 21, 2005, 16:12:42  
Job time : 28 secs

QY 1 CSQNEYFDSLHLHAC---IPCQLRCSSTNP-----PLTCORYC 34  
DB 6 CGENEWLDD---CGTQKPCCAKCNPEEPPEEDPICRSRGC 42

RESULT 75  
US-09-498-556-40  
Sequence 40, Application US/09498556  
Patent No. 6872808

GENERAL INFORMATION:  
APPLICANT: Vlaauk, George Phillip  
Stanssens, Patrick Eric Hugo  
Messens, Joris Hilda Lieven  
Lauwereys, Marc Josef  
Laroche, Yves Rene  
Jespers, Laurent Stephane  
Gansemans, Yannick Georges Jozef  
Moyle, Matthew  
Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
INHIBITORS AND ANTICOAGULANT  
PROTEIN

NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,556  
FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 15:43:09 ; Search time 106.4 Seconds  
(without alignments)  
140.403 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41

Perfect score: 201  
Sequence: 1 CSQNEVFDLSLHACIFCQLRCSNTPTPLTCQRYC 34

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Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	34	AAE15486	Aae15486 Human B-C
2	201	100.0	34	ADA49366	Ada49366 Human BCM
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4	201	100.0	51	AAE15485	Aae15485 Human B-C
5	201	100.0	52	AEC02032	Aec02032 Amino aci
6	201	100.0	58	AAE15501	Aae15501 Human B C
7	201	100.0	181	AAE15484	Aae15484 Human B-C
8	201	100.0	184	AAE08843	Adb08843 Amino aci
9	201	100.0	184	AAE94001	Aay94001 A human B
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11	201	100.0	184	AAE09241	Aay71979 Human B C
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14	201	100.0	184	AAE09241	Adb06098 Human BCM
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18	201	100.0	184	AAE09241	Adb06098 Human BCM
19	201	100.0	184	AAE09241	Adb06098 Human BCM
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23	201	100.0	184	AAE09241	Adb06098 Human BCM
24	201	100.0	184	AAE09241	Adb06098 Human BCM





cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
rheumatoid arthritis; atherosclerosis.

Homo sapiens.  
WO200187979-A2.  
22-NOV-2001.  
14-MAY-2001; 2001WO-US015567.  
12-MAY-2000; 2000US-0204039P.  
27-JUN-2000; 2000US-0214591P.  
14-MAY-2001; 2001US-00214591.  
(AMGE-) AMGEN INC.  
Theill LE, Yu G;  
WPI; 2002-066686/09.  
Inhibiting activity of B cell maturation protein and/or transmembrane  
activator and intracellular cyclophilin ligand interactor, by  
administering a binding partner for APRIL, a tumor necrosis factor family  
ligand.  
Claim 1; Fig 10A; 94pp; English.  
The invention relates to a method for inhibiting TACI (transmembrane  
activator and intracellular CAML interactor) and/or B cell maturation  
protein (BCMA) activity in a mammal. The method comprises administering a  
specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
family ligand), having the consensus region of TACI, BCMA, or the TACI/  
BCMA extracellular consensus sequence, but not the extracellular region  
of TACI or BCMA. The method is useful for inhibiting activity of TACI  
and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
lymphoproliferative disorders, one or more solid tumours such as lung,  
gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
antagonists are useful for treating inflammation and immune function  
diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
disease), drug and insect sting allergy, inflammatory bowel disease  
(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
with leucocyte infiltration of the skin or organs. The present sequence  
is human BCMA protein cysteine-rich consensus region

Sequence 34 AA;  
Query Match 100.0%; Score 201; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34  
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34

RESULT 2  
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AC ADA49366;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human BCMA cysteine rich domain.

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Abp55383 Human col  
Adl15023 Human Igg  
Adq18828 Human sof  
Adv70227 Tumor-ass  
Abg22216 Novel hum  
Aae22261 Human BAF  
Aao21306 Soybean K  
Aaw98909 Mouse IMC  
Aaw98908 Mouse IMC  
Ade25527 Mouse SLP  
Adf28912 Mouse SLP  
Adx02863 Murine an  
Adq59487 Human ca  
Adz13856 Murine ca  
Aae22267 Human BAF  
Adj92151 Human hai  
Adn22513 Bacterial  
Abp34972 Human ORF  
Adf77377 Human tum  
Adj92512 Human TR2  
Aae23295 Human gen  
Aao13678 Human pol  
Abb11195 Human tra  
Aae22254 Human BAF  
Aao21310 Soybean K  
Adx88417 Plant ful  
Adv69654 Human sol  
Ade07963 Novel pro  
Adj92159 Human hai  
Abb62442 Drosophil  
Ady09383 Plant ful  
Abu54212 Human nov  
Abu10466 Novel hum  
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Abu07994 Novel hum  
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Abb66271 Drosophil  
Aar27113 Mj-AMP2 p  
Aar57301 Antimicro  
Aag32139 Dendroasp  
Aay30383 Nematode  
Aay30413 Mature ne  
Aab15298 A. caninu  
Ady37282 Hookworm  
Aar91699 AcanNAPS.  
Aay30394 Nematode

5405 26.6 53.5  
5405 26.6 53.5  
5405 26.6 53.5  
5405 26.6 53.5  
5405 26.6 53.5  
7337 26.6 53.5  
70 26.6 53.5  
108 26.4 53.5  
126 26.4 53.5  
131 26.4 53.5  
131 26.4 53.5  
131 26.4 53.5  
146 26.4 53.5  
146 26.4 53.5  
148 26.4 53.5  
185 26.4 53.5  
271 26.4 53.5  
2824 26.4 53.5  
114 26.1 52.5  
142 26.1 52.5  
142 26.1 52.5  
154 26.1 52.5  
166 26.1 52.5  
976 26.1 52.5  
70 26.1 52.5  
115 26.1 52.5  
133 26.1 52.5  
161 26.1 52.5  
281 26.1 52.5  
292 26.1 52.5  
330 26.1 52.5  
384 26.1 52.5  
547 26.1 52.5  
547 26.1 52.5  
624 26.1 52.5  
624 26.1 52.5  
712 26.1 52.5  
712 26.1 52.5  
780 26.1 52.5  
826 26.1 52.5  
826 26.1 52.5  
904 26.1 52.5  
904 26.1 52.5  
991 26.1 52.5  
991 26.1 52.5  
1069 26.1 52.5  
1069 26.1 52.5  
45 26.1 52.5  
63 26.1 52.5  
63 26.1 52.5  
76 26.1 52.5  
77 26.1 52.5  
77 26.1 52.5  
77 26.1 52.5  
77 26.1 52.5  
100 26.1 52.5  
100 26.1 52.5

ALIGNMENTS

RESULT 1  
AAE15486  
ID AAE15486 standard; peptide; 34 AA.  
XX  
AC AAE15486;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.  
XX  
DE Human; transmembrane activator and intracellular CAML interactor; TACI;  
KW



XX OS Homo sapiens.  
XX PN WO200187979-A2.  
XX PD 22-NOV-2001.  
XX PF 14-MAY-2001; 2001WO-US015567.  
XX PR 12-MAY-2000; 2000US-0204039P.  
XX PR 27-JUN-2000; 2000US-0214591P.  
XX PR 14-MAY-2001; 2001US-00214591.  
XX PA (AMGE-) AMGEN INC.  
XX PI Theill LE, Yu G;  
XX DR WPI; 2002-066686/09.  
XX PT Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX PS Claim 1; Fig 10A; 94pp; English.  
XX CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumor necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, proctitis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human BCMA protein extracellular domain  
XX SQ Sequence 51 AA;  
Query Match 100.0%; Score 201; DB 5; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.2e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEFDSLHLHACIPQLRCSSNTPTLTQRYC 34  
DB 5 CSQNEFDSLHLHACIPQLRCSSNTPTLTQRYC 38  
RESULT 5  
AEC02032  
ID AEC02032 standard; peptide; 52 AA.  
XX AC AEC02032;  
XX DT 20-OCT-2005 (first entry)  
XX DE Amino acid sequence of an extracellular domain of BCMA.  
XX KW APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic;  
KW B-cell maturation antigen; BCMA.  
XX OS Synthetic.  
XX

PN WO2005075511-A1.  
XX 18-AUG-2005.  
XX PF 04-AUG-2004; 2004WO-US025247.  
XX XX 29-JAN-2004; 2004US-0540271P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Kelley RF, Patel D;  
XX DR WPI; 2005-555932/56.  
XX PT New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX PS Disclosure; SEQ ID NO 21; 140pp; English.  
XX CC The specification describes polypeptides that bind April or BAPF. The  
CC polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC scleroma, or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents an extracellular domain of BCMA.  
XX SQ Sequence 52 AA;  
Query Match 100.0%; Score 201; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.3e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEFDSLHLHACIPQLRCSSNTPTLTQRYC 34  
DB 8 CSQNEFDSLHLHACIPQLRCSSNTPTLTQRYC 41  
RESULT 6  
AAE15501  
ID AAE15501 standard; peptide; 58 AA.  
XX AC AAE15501;  
XX DT 12-MAR-2002 (first entry)  
XX DE Human B cell maturation protein cysteine rich extracellular region.  
XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;  
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX OS Homo sapiens.  
XX PN WO200187979-A2.  
XX PD 22-NOV-2001.  
XX PF 14-MAY-2001; 2001WO-US015567.  
XX PR 12-MAY-2000; 2000US-0204039P.  
XX PR 27-JUN-2000; 2000US-0214591P.  
XX PR 14-MAY-2001; 2001US-00214591.  
XX



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XX PN WO200050633-A1.
XX PD 31-AUG-2000.
XX PF 24-FEB-2000; 2000WO-US004925.
XX PR 24-FEB-1999; 99US-0121485P.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Seed B, Ting A;
XX PI WPI; 2000-558405/51.
XX DR
XX PT Identifying a modulator of gene expression for drug designing, by
XX PT contacting a compound library with a cell expressing an anti-cell death
XX PT gene and reporter gene, and determining alteration in reporter gene
XX PT expression.
XX PS
XX PS Claim 32; Fig 7A; 53pp; English.
XX CC
XX CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is
XX CC a necrosis factor (NF)-kB activator. The method of the invention is used
XX CC to identify compounds which modulate BCMA activity (and thus NF-kB
XX CC activity). The specification describes a method of identifying a
XX CC polypeptide which increases gene expression from a promoter. The method
XX CC involves contacting a library of with a cell which expresses a
XX CC recombinant anti-cell death gene and a reporter gene operably linked to
XX CC the promoter, and then determining whether the expression of the reporter
XX CC gene is altered as a result of contact with library. The method is useful
XX CC for identifying polypeptides which increase or decrease gene expression
XX CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
XX CC preparing a pharmaceutical composition for treating cancer, apoptosis,
XX CC viral infections, inflammatory response, such as rheumatoid arthritis,
XX CC inflammatory bowel disease or septic shock. BCMA is useful for
XX CC identifying compounds that modulate NF-kB expression and thus for drug
XX CC designing
XX CC
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
|||||
RESULT 9
AA94001
ID AA94001 standard; protein; 184 AA.
XX AC AA94001;
XX XX
XX DT 20-OCT-2000 (first entry)
XX DE
XX DE A human BCMA protein, a B cell protein related to TACI.
XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX KW ztnf4 activity; antibody production; autoimmunity disease; amyloidosis;
XX KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
XX KW immune response; immunosuppression; graft rejection; joint pain;
XX KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX OS Homo sapiens.

XX PN WO200040716-A2.
XX PD 13-JUL-2000.
XX PF 07-JAN-2000; 2000WO-US000396.
XX PR 07-JAN-1999; 99US-00226533.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Gross JA, Xu W, Madden K, Yee DP;
XX PI WPI; 2000-452538/39.
XX DR N-PSDB; AAA58559.
XX CC
XX CC Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
XX CC renal disease, graft versus host disease, and inflammation, comprises
XX CC administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX PT
XX PS Disclosure; Page 152; 175pp; English.
XX CC
XX CC The present sequence represents a human BCMA protein, a B cell protein
XX CC related to transmembrane activator and CAML-interactor (TACI) receptor.
XX CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX CC protein) receptor contain a cysteine rich domain, and are used for
XX CC inhibiting ztnf4 activity. ztnf4 is a TNF ligand. They may also be used
XX CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
XX CC with activated or resting B lymphocytes, effector T-cells, or with
XX CC antibody production. The antibody production is associated with an
XX CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
XX CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX CC asthma, bronchitis, emphysema, end stage renal failure,
XX CC glomerulonephritis, vasculitis, lymphomas, light chain neuropathy,
XX CC neoplasms, multiple myelomas, lymphomas, immunosuppression, graft
XX CC amyloidosis, moderating immune response, inflammation, insulin dependent
XX CC rejection, graft versus host disease, joint pain, swelling, anaemia, or
XX CC diabetes mellitus, Crohn's disease, and BCMA polypeptides, fusions, antibodies,
XX CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
XX CC agonists or antagonists can be used to treat hypertension, renal artery
XX CC stenosis, or occlusion, and cholesterol or renal emboli
XX CC
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
|||||
RESULT 10
AAE09241
ID AAE09241 standard; protein; 184 AA.
XX AC AAE09241;
XX XX
XX DT 19-NOV-2001 (first entry)
XX DE Human BCMA protein.
XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
XX KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX KW autoimmunity disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX OS Homo sapiens.
XX PN WO200160397-A1.

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PD 23-AUG-2001.  
 XX 28-NOV-2000; 2000WO-US032378.  
 XX 16-FEB-2000; 2000US-0182338P.  
 PR 22-AUG-2000; 2000US-0226986P.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
 PI Yan M;  
 XX WPI; 2001-541628/60.  
 DR N-PSDB; AAD15902.  
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists.  
 XX Example 2; Fig 2; 160pp; English.  
 PS The invention relates to methods of using one or more agonists or  
 XX antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TACI or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or  
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human BCMA protein  
 XX Sequence 184 AA;  
 SQ Query Match 100.0%; Score 201; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17; Indels 0; Gaps 0;  
 Matches 34; Conservative 0; Mismatches 0;  
 QY 1 CSQNEYFDSLHACIPQQLRCSSTNPPLTCQRYC 34  
 |||||  
 DB 8 CSQNEYFDSLHACIPQQLRCSSTNPPLTCQRYC 41  
 RESULT 11  
 AAY71979  
 ID AAY71979 standard; protein; 184 AA.  
 XX AAY71979;  
 AC AAY71979;  
 XX 28-MAR-2001 (first entry)  
 DT Human B cell maturation factor (BCMA) protein.  
 XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;  
 KW Tumour necrosis factor and Apol-related leucocyte expressed Ligand 1;  
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;  
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;  
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;  
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;  
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH Domain 1..62  
 FT /label= Extracellular\_domain  
 XX WO200068378-A1.  
 PN 16-NOV-2000.  
 XX

XX 05-MAY-2000; 2000WO-US012266.  
 PF 06-MAY-1999; 99US-0132892P.  
 PR 01-MAY-2000; 2000US-0201012P.  
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.  
 PA Shu HS;  
 PI WPI; 2001-016094/02.  
 DR N-PSDB; AAD02125.  
 XX Isolated TALL-1 protein is used to identify compounds that regulate B  
 PT lymphocyte proliferation, used to treat B lymphocyte associated  
 PT autoimmune disorders.  
 XX Claim 37; Page 104-105; 112pp; English.  
 PS The present invention relates to Tumour necrosis factor (TNF) and Apol-  
 CC related leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, in  
 CC proteins (including homologues), and their antibodies. The invention, in  
 CC particular relates to methods for regulating the interaction between TALL  
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to  
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.  
 CC TALL-1 protein is useful for identifying compounds that regulate B  
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte  
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus  
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple  
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,  
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal  
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its  
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.  
 CC The present sequence is a human B cell maturation factor (BCMA) protein.  
 CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome  
 CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not  
 CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.  
 CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression  
 CC increases with B lymphocyte maturation  
 XX Sequence 184 AA;  
 SQ Query Match 100.0%; Score 201; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17; Indels 0; Gaps 0;  
 Matches 34; Conservative 0; Mismatches 0;  
 QY 1 CSQNEYFDSLHACIPQQLRCSSTNPPLTCQRYC 34  
 |||||  
 DB 8 CSQNEYFDSLHACIPQQLRCSSTNPPLTCQRYC 41  
 RESULT 12  
 AAB60698  
 ID AAB60698 standard; protein; 184 AA.  
 XX AAB60698;  
 AC AAB60698;  
 XX 22-MAY-2001 (first entry)  
 DT Human BAFF receptor (BAFF-R).  
 DE Human BAFF receptor (BAFF-R).  
 XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
 KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;  
 KW B-cell maturation inhibitor; immunoglobulin production disorder; hypertension;  
 KW autoimmune disorder; B-cell lymphoproliferative disorder; HIV infection;  
 KW renal disorder; immunosuppressive disorder; organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; gene therapy; cancer; tumour.  
 XX Homo sapiens.  
 OS

XX WO200112812-A2.  
XX 22-FEB-2001.  
XX 16-AUG-2000; 2000WO-US022507.  
XX 17-AUG-1999; 99US-0149378P.  
PR 11-FEB-2000; 2000US-0181684P.  
PR 18-FEB-2000; 2000US-0183536P.  
XX (BIOJ ) BIOGEN INC.  
PA (APOT-) APOTECH R & D SA.  
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
PI Thompson J;  
XX WPI; 2001-202866/20.  
DR N-PSDB; AAF59998.  
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
XX Claim 20; Fig 1; 59pp; English.  
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
CC agent, and also plays a role in the development of hypertension and  
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
CC be used in the treatment of immunosuppressive disorders and HIV  
CC infection, and in patients undergoing organ transplantation. The BAFF-R  
CC proteins or BAFF-R specific antibodies may be used for treating,  
CC suppressing or altering an immune response involving a signalling pathway  
CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R  
CC inhibits B-cell growth and maturation it is useful for treating diseases  
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding  
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,  
CC autoimmune disorders and inherited B-cell-associated disorders. The  
CC present sequence represents human BAFF-R  
XX  
XX Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
RESULT 13  
ID AAE00506  
XX AAE00506 standard; protein; 184 AA.  
XX AAE00506;  
XX 31-JUL-2001 (first entry)  
XX Human B cell maturation protein (BCMA).  
XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;  
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;  
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;

KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;  
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;  
KW organ transplantation; HIV; human immunodeficiency virus; TNF;  
KW tumour necrosis factor; BCMA; B cell maturation protein.  
XX Homo sapiens.  
OS WO200124811-A1.  
PN 12-APR-2001.  
XX 05-OCT-2000; 2000WO-US027579.  
XX 06-OCT-1999; 99US-0157933P.  
PR 11-FEB-2000; 2000US-0181807P.  
PR 30-JUN-2000; 2000US-0215688P.  
XX (BIOJ ) BIOGEN INC.  
PA (APOT-) APOTECH R & D SA.  
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
PI WPI; 2001-266242/27.  
XX N-PSDB; AAD03844.  
XX Treating a mammal for a condition associated with undesired cell  
PT proliferation such as cancer or carcinoma, comprises administering a  
PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
PT antagonist.  
XX Claim 3; Fig 3A; 85pp; English.  
XX The invention relates to a method of treating a mammal for a condition  
CC associated with undesired cell proliferation such as cancer or carcinoma.  
CC The method involves administering a composition comprising A  
CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell  
CC maturation protein (BCM or BCMA) antagonist that antagonises the  
CC interaction between APRIL and its cognate receptor(s). This method is  
CC useful for treating undesired cell proliferation such as cancer or  
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,  
CC prostate carcinoma, and other carcinomas whose proliferation is modulated  
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's  
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular  
CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
CC immunosuppressive diseases, organ transplantation, inflammation and human  
CC immunodeficiency virus (HIV), and for treating, suppressing or altering  
CC an immune response involving a signalling pathway between APRIL-R and its  
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
CC is human APRIL-R also referred as BCMA or BCM protein  
XX  
XX Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
RESULT 14  
ID ABB81487  
XX ABB81487 standard; protein; 184 AA.  
XX ABB81487;  
XX 02-SEP-2002 (first entry)  
XX Human BCMA receptor related protein SEQ ID NO:7.  
XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;  
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;

KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;  
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
KW light chain neuropathy; hypertension; large vessel disease;  
KW graft-versus host disease; graft rejection; Crohn's disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200238766-A2.  
XX  
PD 16-MAY-2002.  
XX  
PF 05-NOV-2001; 2001WO-US047018.  
XX  
PR 07-NOV-2000; 2000US-0246449P.  
PR 20-DEC-2000; 2000US-0257131P.  
PR 28-JUN-2001; 2001US-0301715P.  
PR 29-AUG-2001; 2001US-0315565P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Gross JA, Xu W, Henne RM, Grant FJ;  
XX  
XX WPI; 2002-508212/54.  
DR  
XX  
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed  
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
PT renal failure or renal disease and lymphoma.  
XX  
PS Disclosure; Page 135-136; 154pp; English.  
XX  
CC The present invention describes a human tumour necrosis factor receptor  
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
CC antineumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive  
CC activities, and can be used in gene therapy. (I) can be used for  
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12  
CC (e.g. ZTNF4), for treating disorders and diseases associated with B  
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for  
CC inhibiting the proliferation of tumour cells. (I) is useful for treating  
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia  
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,  
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure  
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid  
CC leukaemia, nephritis, and pyelonephritis, and for treating renal  
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or  
CC amyloidosis, hypertension, large vessel diseases, graft-versus host  
CC disease, graft rejection and Crohn's disease. (I) is useful for  
CC modulating the immune system, for regulating B cell responses and  
CC development, for modulating development of other cells, antibody  
CC production and cytokine production, and for modulating T and B cell  
CC communication. The present sequence represents a protein which is given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41  
RESULT 15  
ABP54694  
ID ABP54694 standard; protein; 184 AA.  
XX

AC ABP54694;  
XX  
DT 30-DEC-2002 (first entry)  
XX  
DE Metastatic colorectal cancer-associated polypeptide.  
XX  
KW Colorectal cancer; metastasis; differential expression; cytostatic;  
KW diagnosis; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200268677-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 27-FEB-2002; 2002WO-US006001.  
XX  
PR 27-FEB-2001; 2001US-0272206P.  
PR 02-APR-2001; 2001US-0281149P.  
PR 17-APR-2001; 2001US-0284555P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Mack DH, Markowitz SD;  
XX  
XX WPI; 2002-698677/75.  
DR N-PSDB; ABQ81560.  
XX  
PT New genes that are up- or down-regulated in colorectal cancer, useful for  
PT diagnosing colorectal cancer in a subject, or for identifying modulators  
PT of colorectal cancer-associated proteins and genes for treating  
PT colorectal cancer.  
XX  
PS Claim 8; Page 255; 260pp; English.  
XX  
CC The present sequence is the protein sequence of a human polypeptide  
CC encoded by a gene that exhibits decreased expression in colon cancer-  
CC derived metacases compared to normal colon tissue. It is an example of  
CC claimed polypeptides that are encoded by genes which are differentially  
CC expressed in metastatic colorectal cancer cells. Such polypeptides are  
CC useful in diagnostic and prognostic assays, for raising antibodies useful  
CC e.g. in immunotherapy, and in screening for modulator compounds of  
CC therapeutic value  
XX  
SQ Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41  
RESULT 16  
AAE28961  
ID AAE28961 standard; protein; 184 AA.  
XX  
AC AAE28961;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Human B-cell maturation antigen (BCMA).  
XX  
KW Human; tumour; B-cell maturation antigen; transmembrane activator;  
KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;  
KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;  
KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;  
KW BCMA; multiple myeloma.  
XX  
OS Homo sapiens.



XX FH Key Location/Qualifiers  
 XX FT 1. .54  
 XX FT /note= "Antigenic epitope"  
 XX FT Domain 1. .48  
 XX FT /note= "Extracellular domain"  
 XX FT Region 8. .41  
 XX FT /note= "Cysteine rich region"  
 XX PN WO200266516-A2.  
 XX PD 29-AUG-2002.  
 XX PF 06-FEB-2002; 2002WO-US003500.  
 XX PR 20-FEB-2001; 2001US-0270274P.  
 XX PR 12-APR-2001; 2001US-0283447P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Kindavogel W;  
 XX PS WPI; 2002-723183/78.  
 XX PD N-PSDB; AAD46410.  
 XX PT B-cell maturation antigen and transmembrane activator and calcium-  
 XX PT modulator and cyclophilin ligand-interactor, useful for treating  
 XX PT disorders e.g. inflammation or lymphoma.  
 XX PS Disclosure; Page 63; 67pp; English.  
 XX CC The invention relates to the manufacture of a composition for inhibiting  
 XX CC the proliferation of tumour cells. The method involves using an antibody  
 XX CC component that binds both the B-cell maturation antigen (BCMA) and the  
 XX CC transmembrane activator and calcium-modulator and cyclophilin ligand-  
 XX CC interactor (TACI). BCMA and TACI binding antibody compositions are useful  
 XX CC for inhibiting proliferation of tumour cells, particularly inhibiting  
 XX CC ZTNF4 activity in a mammal associated with increased endogenous antibody  
 XX CC production or a disorder consisting of neoplasia, chronic lymphocytic  
 XX CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation  
 XX CC lymphoproliferative disease or light chain gammopathy or inflammation  
 XX CC e.g. asthma. The invention is also useful in gene therapy. The present is  
 XX CC human BCMA protein  
 XX SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CSQNEYFDSLHLHACIPCOLRCSSTPPLTCQRYC 34  
 Db 8 CSQNEYFDSLHLHACIPCOLRCSSTPPLTCQRYC 41  
 RESULT 17  
 AAEE35216  
 ID AAEE35216 standard; protein; 184 AA.  
 XX AC AAEE35216;  
 XX DT 28-MAY-2003 (first entry)  
 XX DE Human B-cell maturation receptor (BCMA) protein.  
 XX KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;  
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;  
 KW B-cell maturation receptor; BCMA; receptor.

XX OS Homo sapiens.  
 XX PN WO200294852-A2.  
 XX PD 28-NOV-2002.  
 XX PF 20-MAY-2002; 2002WO-US015910.  
 XX PR 24-MAY-2001; 2001US-0293343P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Rixon MW, Gross JA;  
 XX PD WPI; 2003-148455/14.  
 XX PD N-PSDB; AAD53754.  
 XX PT Transmembrane activator and calcium modulator and cyclophilin ligand-  
 XX PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or  
 XX PT diabetes, comprises a TACI receptor group and an immunoglobulin group.  
 XX PS Disclosure; Col 100; 71pp; English.  
 XX CC The invention relates to fusion proteins comprising transmembrane  
 XX CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)  
 XX CC receptor group that binds tumour necrosis factor-like protein (ZTNF2) or  
 XX CC ZTNF4; and an immunoglobulin group comprising a constant region of an  
 XX CC immunoglobulin. The invention is used to manufacture a medicament for  
 XX CC inhibiting the proliferation of tumour cells in a mammalian subject. The  
 XX CC composition comprising the fusion protein may also be used in treating  
 XX CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
 XX CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal  
 XX CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
 XX CC rejection, anaemia and septic shock. The fusion proteins are also used in  
 XX CC gene therapy. The present sequence is human B-cell maturation receptor  
 XX CC (BCMA) protein used in the invention  
 XX SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 6; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CSQNEYFDSLHLHACIPCOLRCSSTPPLTCQRYC 34  
 Db 8 CSQNEYFDSLHLHACIPCOLRCSSTPPLTCQRYC 41  
 RESULT 18  
 ADA49361  
 ID ADA49361 standard; protein; 184 AA.  
 XX AC ADA49361;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Human BCMA protein.  
 XX KW human; TALL-1; antagonist; immunosuppressive; antirheumatic;  
 KW antiinflammatory; antiarthritic; dermatological; antidiabetic;  
 KW neuroprotective; antithyroid; antipruritic; nephrotropic; vasotropic;  
 KW vaccine; autoimmune diseases; rheumatoid arthritis;  
 KW systemic lupus erythematosus; insulin dependent diabetes mellitus;  
 KW multiple sclerosis; myasthenia gravis; Grave's disease;  
 KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;  
 KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;  
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.  
 XX OS Homo sapiens.  
 XX PN WO2003035846-A2.

PD 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348962P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

DR N-PSDB; ADA49360.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological

PT activity in mammal, has a modification in the region connecting beta

PT strands D and E that reduces the biological activity of TALL-1

PT antagonist.

XX Claim 62; Page 613; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a

CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID

CC NO:2, by at least one modification in the region connecting ebgrr; strands

CC D and E that reduces the biological activity of the TALL- 1 antagonist as

CC compared to wild-type TALL-1. A protein of the invention has

CC immunosuppressive, antirheumatic, neuroprotective, antiarthritic,

CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,

CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in

CC a vaccine. A protein of the invention is useful for inhibiting TALL-1

CC biological activity in a mammal. TC is useful for treating autoimmune

CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin

CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,

CC Grave's disease, autoimmune hemolytic anaemia, autoimmune

CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,

CC acute rheumatic fever, post-streptococcal glomerulonephritis and

CC polyarthritis nodosa. The present sequence represents human BCMA.

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 34

|||||

Db 8 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 41

RESULT 19

ABR40082

ID ABR40082 standard; protein; 184 AA.

XX

AC ABR40082;

XX

DT 27-JUN-2003 (first entry)

XX

DE Human Genoxit.

DE

XX Human; genoxit; anorectic; antilipaeamic; antiarteriosclerotic; cardiant;

KW antidiabetic; hypotensive; ophthalmological; neuroprotective;

KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;

KW Type III transmembrane protein; insulin resistance; atherosclerosis;

KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;

KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1..54

FT /label= Extracellular\_domain

FT Misc-difference 3

FT Domain /label= Gln, Lys

FT 55..77

FT /label= Transmembrane domain

FT Domain 78..184

FT /label= Intracellular\_domain

XX WO2003013582-A1.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-IB003498.

XX 06-AUG-2001; 2001US-0310754P.

XX (GEST ) GENSET SA.

XX Lucas J, Dialynas D, Briggs K;

XX WPI; 2003-268160/26.

DR N-PSDB; ACC00340.

XX New use of agonist or antagonist of Genoxit activity for preventing or

PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and

PT atherosclerosis.

XX Disclosure; Page 32; 35pp; English.

XX The present invention relates to the use of an agonist or antagonist of

CC Genoxit activity for preventing or treating obesity. Genoxit is a member

CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III

CC transmembrane protein. The agonists or antagonists of the invention are

CC useful for treating or preventing obesity-related diseases or disorders,

CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,

CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high

CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus

CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic

CC complications, e.g. microangiopathic lesions, ocular lesions,

CC retinopathy, neuropathy and renal lesions

XX

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 34

|||||

Db 8 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 41

RESULT 20

ABP60552

ID ABP60552 standard; protein; 184 AA.

XX

AC ABP60552;

XX

DT 28-MAR-2003 (first entry)

XX

DE Human tumour necrosis factor BCMA.

DE

XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;

KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;

KW antiarthritic; cytostatic; antianaemic; antiallergic; antiaschmatic;

KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;

KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;

KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;

KW inflammatory disorder; proliferative disorder; single chain antibody;

KW antibody; human; BCMA; tumour necrosis factor.

XX

OS Homo sapiens.

XX

PN WO200294192-A2.

XX PD 28-NOV-2002.  
 XX PF  
 XX PR 22-MAY-2002; 2002WO-US016106.  
 XX PR 24-MAY-2001; 2001US-0293100P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Ruben SM;  
 XX PI WPI; 2003-156740/15.  
 XX DR  
 XX PT Novel isolated antibody that immunospecifically binds tumor necrosis  
 PT factor delta, useful for treating, preventing or ameliorating Non-  
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's  
 PT syndrome.  
 XX PS Disclosure; Page 222; 225pp; English.  
 XX CC The invention relates to a novel antibody or its fragment, which  
 CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).  
 CC The antibody of the invention has dermatological, immunosuppressive,  
 CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,  
 CC antiallergic, antisthmatic, neuroprotective, ophthalmological,  
 CC tuberculostatic, antidiabetic, antipeoriatic, anti-HIV,  
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.  
 CC The antibody or its fragment are useful for treating, preventing or  
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in  
 CC human, disease or disorder such as autoimmune disease, and graft versus  
 CC host disease (GVHD). The autoimmune disease is systemic lupus  
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody  
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or  
 CC ameliorating a disease or disorder associated with aberrant APRIL or  
 CC APRIL receptor expression or aberrant function of APRIL or APRIL  
 CC receptor. The disease or disorders includes autoimmune and inflammatory  
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,  
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,  
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune  
 CC system, particularly B cell cancers, immune disorders such as myasthenia  
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,  
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and  
 CC proliferative disorders (e.g. leukemia). The present sequence represents  
 CC the tumour necrosis factor BCMA  
 XX SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 6; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
 DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
 RESULT 21  
 ABP97717  
 ID ABP97717 standard; protein; 184 AA.  
 XX AC ABP97717;  
 XX DT 28-MAY-2003 (first entry)  
 XX DE Amino acid sequence of human BCMA receptor.  
 XX KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus; BCMA.  
 XX OS Homo sapiens.  
 XX PN WO2003014294-A2.  
 XX PT

PD 20-FEB-2003.  
 XX PF 24-JUL-2002; 2002WO-US023487.  
 XX PR 03-AUG-2001; 2001US-0310114P.  
 XX PR 30-APR-2002; 2002US-0377171P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Dixit V, Grewal I, Ridgway J, Yan M;  
 XX PI WPI; 2003-256560/25.  
 XX DR N-PSDB; AB268871.  
 XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
 PT preparing a composition for treating systemic lupus erythematosus.  
 XX PS Disclosure; Fig 2; 153pp; English.  
 XX CC The present sequence represents a human BCMA polypeptide. The  
 CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are  
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April  
 CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to  
 CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for  
 CC preparing a composition for treating systemic lupus erythematosus  
 XX SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 6; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34  
 DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41  
 RESULT 22  
 ADD67527  
 ID ADD67527 standard; protein; 184 AA.  
 XX AC ADD67527;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE Human Ly1732P protein SEQ ID NO:4.  
 XX KW haematological malignancy; immunoconjugate; cytostatic; immunoestimulant;  
 KW vaccine; immunotherapy; cancer; multiple myeloma cell;  
 KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;  
 KW human.  
 XX OS Homo sapiens.  
 XX PN WO2003062401-A2.  
 XX PD 31-JUL-2003.  
 XX PF 22-JAN-2003; 2003WO-US002353.  
 XX PR 22-JAN-2002; 2002US-00057475.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;  
 PI Carter L, McNeill PD;  
 XX WPI; 2003-598749/56.  
 XX DR N-PSDB; ADD67526.  
 XX PT New hematological malignancy-related genes and polypeptides, useful for  
 PT screening anti-cancer agents, and generating antibodies or  
 PT immunoconjugates for treating e.g. multiple myeloma cell or chronic

PT Lymphocytic leukemia.

XX Claim 9; SEQ ID NO 4; 307pp; English.

XX The present invention describes an isolated polynucleotide (I), which is

CC overexpressed in haematological malignancies, and which encodes a

CC polypeptide or an immunogenic fragment of the polypeptide. Also

CC described: (1) an isolated polypeptide; (2) an expression vector

CC comprising (1) operably linked to an expression control sequence; (3) a

CC host cell comprising an expression vector; (4) an isolated antibody that

CC specifically binds to the polypeptide or its immunogenic fragment; and

CC (5) immunocojugates comprising the antibody above, or an antibody that

CC specifically binds to a polypeptide, or its immunogenic fragment, encoded

CC by (1). (I) has cytostatic and immunostimulant activities, and can be

CC used in vaccines and immunotherapy. The immunoconjugates are useful in

CC the manufacture of a medicament, particularly as active ingredients in a

CC composition for treating cancer, e.g. multiple myeloma cell, chronic

CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,

CC primates, goats, bovines, equines, porcines, lupines, canines or felines.

CC The polynucleotide (I) or polypeptide can be used for screening anti-

CC cancer agents, and generating antibodies or immunoconjugates for treating

CC or preventing the above-mentioned diseases. The polynucleotide,

CC polypeptide or antibody can be used for detecting, diagnosing or

CC prognosticating the haematological malignancies described above. The

CC present sequence is used in the exemplification of the present invention.

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 201; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 34

DB 8 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 41

RESULT 23

ADG43715

ID ADG43715 standard; protein; 184 AA.

AC ADG43715;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human B-cell maturation antigen SEQ ID NO:1.

XX human; neurodegenerative immunological disorder; demyelination;

KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;

KW BCMA; multiple sclerosis; neuroprotective; neurotropic; antiinflammatory;

KW gene therapy.

XX

OS Homo sapiens.

XX

PN WO2003072713-A2.

XX

PD 04-SEP-2003.

XX

PF 21-FEB-2003; 2003WO-US005147.

XX

PR 21-FEB-2002; 2002US-0358427P.

XX

PA (BIOJ ) BIOGEN INC.

XX

XX Kalled SL, Reid H;

XX WPI: 2003-721758/68.

DR N-PSDB; ADG43716.

XX

PT Treating a neurodegenerative immunological disorder, e.g. demyelination

PT or inflammation in a mammal comprises administering a B-cell maturation

PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.

XX

PS Claim 8; Page 68-69; 72pp; English.

XX The invention relates to a novel method for treating a neurodegenerative

CC immunological disorder, demyelination or Central Nervous System (CNS)

CC inflammation in a mammal. The method comprises administering B-cell

CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand

CC (the mammal has or is at risk of developing multiple sclerosis). The

CC method of the invention has neuroprotective, neurotropic, and

CC antiinflammatory activity, and may have a use in gene therapy. The

CC methods, BCMA, and antibodies are useful for treating a neurodegenerative

CC immunological disorder such as multiple sclerosis, demyelination or CNS

CC inflammation. The present sequence represents human BCMA.

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 201; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 34

DB 8 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 41

RESULT 24

ADK00756

ID ADK00756 standard; protein; 184 AA.

XX

AC ADK00756;

XX

DT 06-MAY-2004 (first entry)

XX

DE Native human BCMA.

XX

KW CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;

KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;

KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;

KW Antibacterial; antiparasitic; systemic lupus erythematosus;

KW diabetes mellitus; AIDS; BCMA.

XX

OS Homo sapiens.

XX

PN WO2004011611-A2.

XX

PD 05-FEB-2004.

XX

PF 25-JUL-2003; 2003WO-US023421.

XX

PR 25-JUL-2002; 2002US-0398530P.

XX

PA (GETH ) GENENTECH INC.

XX

XX Chuntharapai A, Grewal I, Kim KJ, Yan M;

PI WPI: 2004-143841/14.

DR N-PSDB; ADK00755.

XX

PT New anti-TACI receptor monoclonal antibody, useful for diagnosing and

PT treating pathological conditions associated with tumor necrosis factor,

PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or

PT psoriasis.

XX

PS Disclosure; SEQ ID NO 6; 110pp; English.

XX

CC The present invention relates to an isolated monoclonal antibody which

CC binds to a transmembrane activator of and CAML interactor (TACI)

CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI

CC polypeptide biological activity in mammalian cells, or for diagnosing and

CC treating pathological conditions associated with TNF and TNF receptor-

CC related molecules, e.g. cancer or immune-related disease, such as

CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,

CC systemic vasculitis, diabetes mellitus, Crohn's disease,

CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or

CC infectious diseases including AIDS, hepatitis infection, bacterial  
 CC infection, fungal infection, protozoal infection and parasitic infection.  
 CC The present sequence represents native human BCMA.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 25  
 ADQ94442  
 ID ADQ94442 standard; protein; 184 AA.

XX ADQ94442;

AC 07-OCT-2004 (first entry)

XX Neurokine-alpha, BCMA.

XX neurokine-alpha; chelator; B-lymphocyte stimulator; BLYS; TALL-1; THANK;  
 KW BAPF; neurokine-alpha receptor; complex; metal ion; radiotherapy;  
 KW B-cell mediated disease; non-Hodgkin's lymphoma;  
 KW chronic lymphocytic leukaemia; multiple myeloma;  
 KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;  
 KW Crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis;  
 KW asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte;  
 KW B cell; cancerous cell; metastasis; lymphatic system.

XX Homo sapiens.

XX WO2004058309-A1.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040979.

XX 23-DEC-2002; 2002US-0435262P.

XX 02-MAY-2003; 2003US-0467198P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Parmelee D, Yeh R, Galperina O, Hilbert D, Rosen CA;

XX WPI; 2004-553134/53.

XX N-PSDB; ADQ94441.

XX GENBANK; NM\_001192.

XX Neurokine-alpha conjugate useful for targeting complexed metal ion to  
 PT cells expressing receptor (predominantly lymphoid) for radiotherapy  
 PT treatment of, for example, non-Hodgkin's lymphoma comprises neurokine-  
 PT alpha protein and chelator.

XX Disclosure; SEQ ID NO 9; 228pp; English.

XX This sequence represents neurokine-alpha, BCMA, which may be used in the  
 CC protein conjugate of the invention. The neurokine-alpha protein  
 CC conjugate comprises neurokine-alpha protein and chelator, where the  
 CC neurokine-alpha protein (also known as B-lymphocyte stimulator (BLYS),  
 CC TALL-1, THANK and BAPF) is capable of binding neurokine-alpha receptor  
 CC and is selected from full length or mature neurokine-alpha protein. The  
 CC protein conjugate of the invention is useful in a complex with a metal  
 CC ion associated with the chelator which is useful for administering  
 CC radiotherapy to a subject such as human who is in need of radiotherapy,  
 CC which involves administering the complex to the subject, where it is  
 CC administered as an injectable solution, and the subject has a B-cell  
 CC mediated disease. The subject has a condition chosen from non-Hodgkin's  
 CC lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease,  
 CC diabetes, Wegener's granulomatosis, myasthenia gravis and asthma,  
 CC preferably non-Hodgkin's lymphoma. The complex is useful for treating  
 CC cancer, which involves administering it to a subject having cancer, where  
 CC a cell of the cancer expresses a neurokine-alpha receptor on its  
 CC surface. The cancer is a B cell cancer, which is chosen from non-  
 CC Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia.  
 CC The complex is also useful for treating an autoimmune disease or  
 CC disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis  
 CC and Sjogren's syndrome. The complex may also be used for diagnostic  
 CC imaging. A composition comprising the protein conjugate or the complex is  
 CC useful for killing a cell chosen from a cell bearing a neurokine-alpha  
 CC receptor, and a cell in close proximity to a cell bearing neurokine-  
 CC alpha receptor, which involves contacting the cell with the composition  
 CC to kill the cell. The cell is lymphocyte, B cell or cancerous cell that  
 CC has metastasised into the lymphatic system.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 26

ADP56014

ID ADP56014 standard; protein; 184 AA.

XX ADP56014;

XX 18-NOV-2004 (first entry)

XX Human PRO protein sequence SEQ ID NO:1990.

XX human; PRO; immune related disease; inflammatory immune response;  
 KW immune response stimulation; antiallergic; antianaemic; antiarthritic;  
 KW antidiabetic; antidiabetic; antiinflammatory; antipsoriatic;  
 KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
 KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
 KW virucide; gene therapy.

XX Homo sapiens.

XX WO2004039956-A2.

XX 13-MAY-2004.

XX 28-OCT-2003; 2003WO-US034381.

XX 29-OCT-2002; 2002US-0422472P.

XX (GETH ) GENENTECH INC.

XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
 XX Wood WI, Wu TD;

XX WPI; 2004-376182/35.

XX N-PSDB; ADP56013.

XX New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
 CC and treating an immune related disease, e.g. systemic lupus  
 CC erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
 CC stimulating an immune response.

XX Claim 1; SEQ ID NO 1990; 3009pp; English.

XX The present invention describes an isolated PRO nucleic acid (1). Also  
 CC described: (1) a vector comprising (1); (2) a host cell comprising the

CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
 CC antibody which specifically binds to a polypeptide of (4); (7) a  
 CC composition of matter comprising a polypeptide of (4), an agonist or  
 CC antagonist of the polypeptide or an antibody that binds to the  
 CC polypeptide in combination with a carrier; (8) an article of manufacture  
 CC comprising a container, a label on the container and a composition of  
 CC matter of (7); (9) a method of treating an immune related disease in a  
 CC mammal; (10) a method for determining the presence of a PRO polypeptide  
 CC in a sample suspected of having the polypeptide; (11) a method of  
 CC diagnosing an immune related disease or an inflammatory immune response  
 CC in a mammal; (12) a method of identifying a compound that inhibits or  
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
 CC ; and (13) a method of stimulating the immune response in a mammal. The  
 CC PRO sequences have anti-allergic, anti-inflammatory, antiarthritic,  
 CC antirheumatic, antidiabetic, antitumorigenic, antipsoriatic,  
 CC antihemostatic, hepatotropic, immunostimulant, immunosuppressive,  
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 CC virucide activities, and can be used in gene therapy. The nucleic acid  
 CC (1) and the encoded polypeptides, compositions, kits and methods are  
 CC useful in diagnosing and treating an immune related disease and in  
 CC stimulating an immune response. The present sequence represents a human  
 CC PRO protein from the present invention.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 27  
 ADW03432

ID ADW03432 standard; protein; 184 AA.

XX

AC ADW03432;

DT 24-MAR-2005 (first entry)

XX Human BCMA protein amino acid sequence.

XX B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;  
 KW non-hodgkin lymphoma; hodgkins disease; cytostatic;  
 KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; systemic lupus erythematosus;  
 KW wegener granulomatosis; antiallergic; antinflammatory; vasotropic;  
 KW inflammatory bowel disease; gastrointestinal-gen.;  
 KW idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;  
 KW asthma; antiasthmatic; psoriasis; antipsoriatic; myasthenia gravis;  
 KW muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;  
 KW glomerulonephritis; nephrotropic; BCMA.

OS Homo sapiens.

XX WO200500351-A2.

PN 06-JAN-2005.

XX 04-JUN-2004; 2004WO-US017693.

XX 05-JUN-2003; 2003US-0476414P.

PR 05-JUN-2003; 2003US-0476481P.

PR 06-JUN-2003; 2003US-0476531P.

XX (GETH ) GENENTECH INC.

XX Chan A, Gong Q, Martin F;

XX WPI; 2005-058069/06.  
 DR N-PSDB; ADW03431.

XX Depleting B cells from a mixed population of cells by contacting the  
 PT cells with a Blys antagonist and a CD20 binding antibody, useful for  
 PT treating B cell malignancies and autoimmune disorders.

XX Disclosure; Fig 2; 114pp; English.

XX The invention comprises a method of depleting B cells from a mixed  
 CC population of cells, the method involves contacting the mixed population  
 CC of cells with Blys antagonist (e.g. an immunoadhesin) and a CD20 binding  
 CC antibody (e.g. hu2H7.v16). The method of the invention is useful for  
 CC treating B cell malignancies and autoimmune disorders, such as: non-  
 CC Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas,  
 CC lymphocytic leukemia, Hairy cell leukemia, rheumatoid arthritis, systemic  
 CC lupus erythematosus, Wegener's disease, inflammatory bowel disease,  
 CC idiopathic thrombocytopenic purpura, multiple sclerosis, asthma,  
 CC psoriasis, IGA nephropathy, myasthenia gravis, vasculitis, diabetes and  
 CC glomerulonephritis. The present amino acid sequence represents a human  
 CC BCMA protein.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 9; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 28

ADZ67760

ID ADZ67760 standard; protein; 184 AA.

XX

AC ADZ67760;

DT 14-JUL-2005 (first entry)

XX Human tumor necrosis factor receptor BCMA.

XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;

XX cytostatic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 6..45 /note= "Cys-rich domain"

XX WO2005037865-A2.

XX 28-APR-2005.

XX 18-OCT-2004; 2004WO-US034375.

XX 16-OCT-2003; 2003US-0511698P.

PR 18-OCT-2004; 2004US-0619552P.

XX (Zymo ) ZYMOGENETICS INC.

XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;

XX WPI; 2005-315682/32.

XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
 PT detecting ligands, and for modulating tumor growth, metastasis and  
 PT immunity, such as separating resting from stimulated immune cells.  
 XX Disclosure; SEQ ID NO 8; 132pp; English.

The invention provides novel tumor necrosis factor receptor ztnfr14 polynucleotides AD267753 and polypeptides AD267754, expression vectors and antibodies. Ztnfr14 polynucleotides are used in claimed methods for detecting a genetic abnormality in a patient and for detecting a cancer in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a toxin, is used in a claimed method of killing cancer cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and antagonists. The polypeptides, polynucleotides and antibodies may also be used in methods that modulate tumor growth, metastasis, and immunity such as separating resting from stimulated immune cells. The present sequence is that of human TNFR BCMA. This sequence was compared with that of ztnfr14 in the identification of ztnfr14 as a member of the TNFR family.

XX XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. NO. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
|||||  
DB 8 CSNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41

RESULT 29  
AEA23348  
ID AEA23348 standard; protein; 184 AA.  
XX AC AEA23348;  
DT 11-AUG-2005 (first entry)  
XX DE Tumor antigen of hematopoietic origin TAHO23.  
XX KW cytostatic; gene therapy; therapy: cell growth; protein purification;  
KW DNA purification; hyperproliferation; neoplasm;  
XX tumor antigen of hematopoietic origin; TAHO23.  
XX OS Homo sapiens..  
XX PN W02005049075-A2.  
PD 02-JUN-2005.  
XX PF 16-NOV-2004; 2004WO-US038262.  
XX PR 17-NOV-2003; 2003US-0520842P.  
PR 24-DEC-2003; 2003US-0532426P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Crowley C, Desauvage FJ, Eaton DL, Ebens A, Polson A, Smith V;  
XX WPI; 2005-405198/41.  
DR N-PSDB; AEA23347.  
XX PT Inhibiting the growth of a cell that expresses a protein by contacting  
PT the cell with anti-tumor antigens of hematopoietic origin (TAHO)  
PT polypeptide, antibody or organic molecule, useful for treating  
PT hematopoietic and malignant tumors.  
XX PS Disclosure; SEQ ID NO 46; 367pp; English.  
XX CC The invention describes a method of inhibiting the growth of a cell that  
CC expresses a protein comprising contacting the cell with an antibody,  
CC oligopeptide or organic molecule that binds to the protein, the binding  
CC of the antibody, oligopeptide or organic molecule to the protein and  
CC causing an inhibition of growth of the cell. Also described is a method  
CC for treating or preventing a cell proliferative disorder associated with  
CC increased expression or activity of a protein having at least 80 % amino  
CC acid sequence identity to: a polypeptide having any of SEQ ID NO: 2, 8,  
CC 10, 12, 16, 20, 22, 49 and 51; a polypeptide having the amino acid

SQ Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCRLCSSNTPLTCQRYC 34  
|||||  
DB 8 CSQNEYFDSLHACIPQCRLCSSNTPLTCQRYC 41  
|||||

RESULT 31  
AAE15488  
ID AAE15488 standard; protein; 283 AA.  
XX  
AC AAE15488;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human BCMA-immunoglobulin Fc region fusion protein.  
XX  
KW Human; transmembrane activator and intracellular CAML interactor; TAC1;  
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis; fusion protein.  
XX  
OS Homo sapiens.  
XX  
PN WO200187979-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Theill LE, Yu G;  
XX  
DR WPI; 2002-066686/09.  
XX  
PT Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10B; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TAC1 (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence

CC is human BCMA protein-immunoglobulin Fc region fusion protein  
XX  
SQ Sequence 283 AA;  
Query Match 100.0%; Score 201; DB 5; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2.4e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCRLCSSNTPLTCQRYC 34  
|||||  
DB 5 CSQNEYFDSLHACIPQCRLCSSNTPLTCQRYC 38  
|||||

RESULT 32  
ABG95060  
ID ABG95060 standard; protein; 288 AA.  
XX  
AC ABG95060;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE Human translocation (4; 16)(q26; p13) protein.  
XX  
KW Chromosome aberration; oncogenic fusion protein; cancer;  
KW proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection.  
XX  
OS Homo sapiens.  
XX  
PN WO200269900-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 01-MAR-2002; 2002WO-US006518.  
XX  
PR 01-MAR-2001; 2001US-0272751P.  
XX  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
XX  
PI Fritz LC, Burrows FJ;  
XX  
DR WPI; 2002-698710/75.  
XX  
DR N-PSDB; ABS73235.  
XX  
PT Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX  
PS Disclosure; Page 189-190; 389pp; English.  
XX  
CC The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and



CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents a protein encoded by the DNA sequence of a  
CC chromosome aberration  
XX  
SQ Sequence 288 AA;  
Query Match 100.0%; Score 201; DB 5; Length 288;  
Best Local Similarity 100.0%; Pred. No. 2.4e-17; Indels 0; Gaps 0;  
Matches 34; Conservative 0; Mismatches 0;  
QY 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34  
DB 112 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 145  
RESULT 33  
AAB60699  
ID AAB60699 standard; protein; 302 AA.  
XX  
AC AAB60699;  
XX  
DT 11-SEP-2003 (revised)  
DT 22-MAY-2001 (first entry)  
DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.  
XX  
XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
KW immune-related disorder; B-cell growth inhibitor;  
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
KW autoimmunity disorder; B-cell lymphoproliferative disorder; hypertension;  
KW renal disorder; immunosuppressive disorder; HIV infection;  
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
XX WO200112812-A2.  
XX  
XX 22-FEB-2001.  
XX  
XX 16-AUG-2000; 2000WO-US022507.  
XX  
XX 17-AUG-1999; 99US-0149378P.  
XX 11-FEB-2000; 2000US-0181684P.  
XX 18-FEB-2000; 2000US-0183536P.  
XX  
XX (BIOJ) BIOGEN INC.  
XX (APOT-) APOTEC R & D SA.  
XX  
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
XX Thompson J;  
XX  
XX WPI; 2001-202866/20.  
XX N-PSDB; AAF59999.  
XX  
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
XX lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
XX chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
XX  
XX Example 4; Fig 2; 59pp; English.  
XX  
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
XX treatment of a variety of immune-related disorders. BAFF-R is a member of  
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
XX agent, and also plays a role in the development of hypertension and  
XX related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
XX specific antibodies can be used for inhibiting B-cell growth, dendritic  
XX cell-induced B-cell growth and maturation, and immunoglobulin production,

CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
CC be used in the treatment of immunosuppressive disorders and HIV  
CC infection, and in patients undergoing organ transplantation. The BAFF-R  
CC proteins or BAFF-R specific antibodies may be used for treating,  
CC suppressing or altering an immune response involving a signalling pathway  
CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R  
CC inhibits B-cell growth and maturation it is useful for treating diseases  
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding  
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,  
CC autoimmune disorders and inherited B-cell-associated disorders. The  
CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,  
CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human  
CC BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 302 AA;  
Query Match 100.0%; Score 201; DB 4; Length 302;  
Best Local Similarity 100.0%; Pred. No. 2.6e-17; Indels 0; Gaps 0;  
Matches 34; Conservative 0; Mismatches 0;  
QY 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34  
DB 31 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 64  
RESULT 34  
AAE00507  
ID AAE00507 standard; protein; 302 AA.  
XX  
AC AAE00507;  
XX  
DT 11-SEP-2003 (revised)  
DT 31-JUL-2001 (first entry)  
DE Human BCMA-Immunoglobulin G Fc region fusion construct.  
XX  
XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;  
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;  
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;  
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;  
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;  
KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;  
KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;  
KW immunoglobulin G; IgG; Fc region.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
XX Protein 1..22 /label= Signal peptide  
XX /note= "Derived from murine Ig kappa sequence"  
XX Protein 23..302 /label= Mature human BCMA-IgG\_Fc\_fusion\_protein  
XX /note= "Derived from human BCMA protein"  
XX Region 23..75 /label= Cysteine rich domain  
XX Domain 24..302 /note= "Derived from human BCMA"  
XX Region 76..302 /note= "Derived from human IgG Fc region"  
XX  
XX WO200124811-A1.  
XX  
XX 12-APR-2001.  
XX  
XX 05-OCT-2000; 2000WO-US027579.

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PR 06-OCT-1999; 99US-0157913P.
PR 11-FEB-2000; 2000US-0181807P.
PR 30-JUN-2000; 2000US-0215688P.
XX
XX (BIOJ ) BIOGEN INC.
PA (APOT-) APOTECH R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX
XX WPI; 2001-266242/27.
DR N-PSDB; AAD03847.
DR
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
XX antagonist.
XX
XX Example 1; Fig 3B; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
XX maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and human
XX immunodeficiency virus (HIV), and for treating, suppressing or altering
XX an immune response involving a signalling pathway between APRIL-R and its
XX ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
XX is a fusion construct containing human APRIL-R also referred as BCMA or
XX BCM protein, FC region of human immunoglobulin G (IgG) and a signal
XX sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX
SQ Sequence 302 AA;
Query Match 100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIFCQLRCSSNTPLTCQRYC 34
|||
DB 31 CSQNEYFDSLHACIFCQLRCSSNTPLTCQRYC 64
|||

RESULT 35
ADG43717
ID ADG43717 standard; protein; 302 AA.
XX
XX ADG43717;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human B-cell maturation antigen-Fc SEQ ID NO:3.
DE
DE human; neurodegenerative immunological disorder; demyelination;
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
KW gene therapy; mouse.
XX
XX Chimeric.
OS Homo sapiens.
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 1..23
FT /note= "Murine IgGkappa signal sequence"
FT

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FT Region 24..74
FT /note= "Human BCMA extracellular domain"
FT Region 75..302
FT /note= "Human Ig heavy chain Fc region"
XX
XX WO2003072713-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005147.
XX
XX 21-FEB-2002; 2002US-0358427P.
XX (BIOJ ) BIOGEN INC.
XX
XX Kalled SL, Reid H;
XX
XX WPI; 2003-721758/68.
DR N-PSDB; ADG43718.
DR
XX Treating a neurodegenerative immunological disorder, e.g. demyelination
XX or inflammation in a mammal comprises administering a B-cell maturation
XX antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
XX Claim 12; Page 70-71; 72pp; English.
XX
XX The invention relates to a novel method for treating a neurodegenerative
XX immunological disorder, demyelination or Central Nervous System (CNS)
XX inflammation in a mammal. The method comprises administering B-cell
XX maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
XX (the mammal has or is at risk of developing multiple sclerosis). The
XX method of the invention has neuroprotective, nontropic, and
XX antiinflammatory activity, and may have a use in gene therapy. The
XX methods, BCMA, and antibodies are useful for treating a neurodegenerative
XX immunological disorder such as multiple sclerosis, demyelination or CNS
XX inflammation. The present sequence is used in the exemplification of the
XX invention.
XX
SQ Sequence 302 AA;
Query Match 100.0%; Score 201; DB 7; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIFCQLRCSSNTPLTCQRYC 34
|||
DB 31 CSQNEYFDSLHACIFCQLRCSSNTPLTCQRYC 64
|||

RESULT 36
AEC02026
ID AEC02026 standard; peptide; 34 AA.
XX
XX AEC02026;
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula II derived polypeptide E that binds BAFF.
DE
DE APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
OS
XX WO2005075511-A1.
PN
XX 18-AUG-2005.
PD
XX 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX
XX (GETH ) GENENTECH INC.
PA

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```
Db      1 CSQNEFDSLHLHACIPQLRCSSNTPLTCQRYC 34
|||||
RESULT 39
AEC02017
ID AEC02017 standard; peptide; 34 AA.
XX
AC AEC02017;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula I derived polypeptide F that binds APRIL.
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PN New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Claim 7; SEQ ID NO 6; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
SQ Sequence 34 AA;
XX
Query Match 96.5%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 2e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CSQNEFDSLHLHACIPQLRCSSNTPLTCQRYC 34
Db 1 CSQNEFDSLHLHACKPQLRCSSNTPLTCQRYC 34
|||||
RESULT 40
AEC02042
ID AEC02042 standard; protein; 296 AA.
XX
AC AEC02042;
XX
DT 20-OCT-2005 (first entry)
XX
DE Amino acid sequence of a BCMA-Fc fusion protein.
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;
KW B-cell maturation antigen; Fc.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PN New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
PS Example 6; SEQ ID NO 31; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a BCMA-Fc fusion protein, where 122 of BCMA is changed to Lys.
XX
SQ Sequence 296 AA;
XX
Query Match 96.5%; Score 194; DB 9; Length 296;
Best Local Similarity 97.1%; Pred. No. 2e-16;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CSQNEFDSLHLHACIPQLRCSSNTPLTCQRYC 34
Db 21 CSQNEFDSLHLHACKPQLRCSSNTPLTCQRYC 54
|||||
RESULT 41
AEC02025
ID AEC02025 standard; peptide; 34 AA.
XX
AC AEC02025;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide D that binds BAFF.
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
```

PI Kelley RF, Patel D;  
XX WPI; 2005-555932/56.  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 14; 140pp; English.  
PS  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents a polypeptide of the invention, derived from formula II (see  
CC AEC02021), that that bind BAFF.  
XX  
XX Sequence 34 AA;  
SQ

Query Match 95.5%; Score 192; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 4e-17; 1; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPPLTCQRYC 34  
DB 1 CSQNEAFDLSLLHACIPQLRCSSNTPPLTCQRYC 34  
RESULT 42  
AEC02024  
ID AEC02024 standard; peptide; 34 AA.  
XX  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Formula II derived polypeptide C that binds BAFF.  
XX  
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
XX Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX 18-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 13; 140pp; English.  
PS  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents a polypeptide of the invention, derived from formula II (see  
CC AEC02021), that that bind BAFF.  
XX  
XX Sequence 34 AA;  
SQ

Query Match 95.5%; Score 192; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 4.4e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SQNEVFDLSLLHACIPQLRCSSNTPPLTCQRYC 34  
DB 1 CSQNEAFDLSLLHACIPQLRCSSNTPPLTCQRYC 34  
RESULT 43  
AEC02033  
ID AEC02033 standard; peptide; 38 AA.  
XX  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Amino acid sequence of an extracellular domain of BCMA.  
XX  
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic;  
KW B-cell maturation antigen; BCMA.  
XX  
XX Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX 18-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Disclosure; SEQ ID NO 22; 140pp; English.  
XX  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents an extracellular domain of BCMA.  
XX  
XX Sequence 38 AA;  
SQ

```
Db      1 SQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 33

RESULT 44
AEC02020
ID AEC02020 standard; peptide; 34 AA.
XX
XX AEC02020;
AC
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula I derived polypeptide I that binds APRIL.
DE
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
OS
XX WO2005075511-A1.
PN
XX 18-AUG-2005.
PD
XX
XX 04-AUG-2004; 2004WO-US025247.
PF
XX
XX 29-JAN-2004; 2004US-0540271P.
PR
XX (GETH ) GENENTECH INC.
PA
XX Kelley RF, Patel D;
PI
XX WPI; 2005-555932/56.
DR
XX
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 7; SEQ ID NO 9; 140pp; English.
PS
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
XX Sequence 34 AA;
SQ
Query Match 95.0%; Score 191; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 5.3e-17;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX
XX 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
Db      1 CSQNEYFDSLHACKPCQLRCSSTNPPLTCQRYC 34

RESULT 45
AEC02018
ID AEC02018 standard; peptide; 34 AA.
XX
XX AEC02018;
AC
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula I derived polypeptide G that binds APRIL.
DE
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
```

```
XX
OS Synthetic.
XX PN WO2005075511-A1.
XX PD 18-AUG-2005.
XX PF 04-AUG-2004; 2004WO-US025247.
XX PR 29-JAN-2004; 2004US-0540271P.
XX PA (GETH ) GENENTECH INC.
XX PI Kelley RF, Patel D;
XX DR WPI; 2005-555932/56.
XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 7; SEQ ID NO 7; 140pp; English.
PS
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC sclerosis; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
XX Sequence 34 AA;
SQ
Query Match 94.0%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.6e-17;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX
XX 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34
Db      1 CSQNEYFDSLHACKPCQLRCSSTNPPLTCQRYC 34

RESULT 46
AEC02029
ID AEC02029 standard; peptide; 34 AA.
XX
XX AEC02029;
AC
XX
XX 20-OCT-2005 (first entry)
XX
XX Formula II derived polypeptide H that binds BAFF.
DE
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
XX Synthetic.
OS
XX WO2005075511-A1.
PN
XX 18-AUG-2005.
PD
XX 04-AUG-2004; 2004WO-US025247.
PF
XX 29-JAN-2004; 2004US-0540271P.
PR
XX (GETH ) GENENTECH INC.
PA
XX Kelley RF, Patel D;
XX
```

DR WPI; 2005-555932/56.  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX Claim 13; SEQ ID NO 18; 140pp; English.  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents a polypeptide of the invention, derived from formula II (see  
 CC AEC02021), that that bind BAFF.  
 XX Sequence 34 AA;  
 SQ

Query Match 94.0%; Score 189; DB 9; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 9.6e-17;  
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34  
 |||||  
 Db 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34  
 |||||

RESULT 47  
 AEC02019  
 ID AEC02019 standard; peptide; 34 AA.  
 XX AC AEC02019;  
 XX DT 20-OCT-2005 (first entry)  
 XX DE Formula I derived polypeptide H that binds APRIL.  
 XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
 KW Synthetic.  
 OS WO2005075511-A1.  
 XX PN 18-AUG-2005.  
 XX PD 04-AUG-2004; 2004WO-US025247.  
 XX PF 29-JAN-2004; 2004US-0540271P.  
 XX PR (GETH ) GENENTECH INC.  
 XX PA Kelley RF, Patel D;  
 XX PI WPI; 2005-555932/56.  
 XX DR New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX Claim 7; SEQ ID NO 8; 140pp; English.  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents polypeptide of the invention that binds APRIL, derived from  
 CC AEC02012.  
 XX Sequence 34 AA;  
 SQ

Query Match 90.5%; Score 182; DB 9; Length 34;  
 Best Local Similarity 91.2%; Pred. No. 7.5e-16;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34  
 |||||  
 Db 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34  
 |||||

RESULT 48  
 AAB60700  
 ID AAB60700 standard; protein; 157 AA.  
 XX AC AAB60700;  
 XX DT 22-MAY-2001 (first entry)  
 XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.  
 XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
 KW immune-related disorder; B-cell growth inhibitor; BCMA;  
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
 KW renal disorder; immunosuppressive disorder; HIV infection;  
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.  
 XX OS Homo sapiens.  
 XX PN WO200112812-A2.  
 XX PD 22-FEB-2001.  
 XX PF 16-AUG-2000; 2000WO-US022507.  
 XX PR 17-AUG-1999; 99US-0149378P.  
 XX PR 11-FEB-2000; 2000US-018184P.  
 XX PR 18-FEB-2000; 2000US-0183536P.  
 XX PA (BIOJ ) BIOGEN INC.  
 XX PA (APOT-) APOTEC R & D SA.  
 XX PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
 XX Thompson J;  
 XX WPI; 2001-202866/20.  
 XX DR N-PSDB; AAF60000.  
 XX PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
 XX Example 1; Fig 3; 59pp; English.  
 XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
 CC agent, and also plays a role in the development of hypertension and  
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also

CC be used in the treatment of immunosuppressive disorders and HIV  
 CC infection, and in patients undergoing organ transplantation. The BAPF-R  
 CC proteins or BAPF-R specific antibodies may be used for treating,  
 CC suppressing or altering an immune response involving a signalling pathway  
 CC between BAPF-R and BAPF, thereby inhibiting inflammation. Since BAPF-R  
 CC inhibits B-cell growth and maturation it is useful for treating diseases  
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding  
 CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,  
 CC autoimmune disorders and inherited B-cell-associated disorders. The  
 CC present sequence represents a human BAPF-R protein sequence as encoded by  
 CC plasmid pJST535. However, this BAPF-R protein sequence is 27 amino acids  
 CC shorter than that given in AAB60698  
 CC  
 XX Sequence 157 AA;

Query Match 79.4%; Score 159.5; DB 4; Length 157;  
 Best Local Similarity 90.6%; Pred. No. 2.6e-12;  
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 QNEYFDSLLHACIPCQLRCSSTNPPLTCQRYC 34  
 DB 7 QNEYFDSLLHACIPCQLR---NTPPLTCQRYC 35

RESULT 49  
 ADI53060  
 ID ADI53060 standard; peptide; 26 AA.

AC ADI53060;

XX 22-APR-2004 (first entry)

DE Human BCMA receptor binding site.

XX protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;  
 KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;  
 KW antidiabetic; dermatological; antiasthmatic; neurokine-alpha;  
 KW crystallography; cancer; allergic disorder; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;  
 KW systemic lupus erythematosus; asthma; receptor.

XX Homo sapiens.

XX WO2003050134-A2.

XX 19-JUN-2003.

XX 07-NOV-2002; 2002WO-US035661.

XX 07-NOV-2001; 2001US-0331049P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Li Y, Oren DE, Arnold E, Volevok Y;

XX WPI; 2003-532895/50.

XX New crystalline Neurokine-alpha protein, useful for designing compounds  
 PT that bind, inhibit or mimic a Neurokine-alpha protein or enhance the  
 PT activity of a Neurokine-alpha protein for treating e.g. cancer or  
 PT allergic disorders.

XX Disclosure; Fig 4; 362pp; English.

XX The invention relates to a neurokine-alpha protein in crystalline form.  
 CC The crystalline neurokine-alpha protein is useful for designing  
 CC molecules that have biological activity or compounds that bind, inhibit  
 CC or mimic a neurokine-alpha protein and/or enhance the activity of a  
 CC neurokine-alpha protein. The three-dimensional structure of a neurokine  
 CC -alpha protein is useful in determining the three-dimensional of other  
 CC neurokine-alpha proteins and their homologs. The compounds that mimic,

CC prevent or inhibit the activity of the protein are useful for treating  
 CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid  
 CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus  
 CC erythematosus or asthma. This sequence represents the residues in the  
 CC receptor for binding a cytokine ligand.

XX Sequence 26 AA;

Query Match 75.1%; Score 151; DB 7; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-12;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYFDSLLHACIPCQLRCSSTNPPLTC 30  
 DB 1 EYFDSLLHACIPCQLRCSSTNPPLTC 26

RESULT 50

AAB08844

ID AAB08844 standard; peptide; 185 AA.

XX AAB08844;

XX 02-JAN-2001 (first entry)

DE Amino acid sequence of murine BCMA polypeptide.

XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;  
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;  
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX Mus musculus.

XX Key Location/Qualifiers

XX Domain 47..72

XX /note= "putative transmembrane domain"

XX WO2000050633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-US004925.

XX 24-FEB-1999; 99US-0121485P.

XX (GEHO ) GEN HOSPITAL CORP.

XX Seed B, Ting A;

XX WPI; 2000-558405/51.

XX Identifying a modulator of gene expression for drug designing, by  
 PT contacting a compound library with a cell expressing an anti-cell death  
 PT gene and reporter gene, and determining alteration in reporter gene  
 PT expression.

XX Claim 32; Fig 7B; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is  
 CC a necrosis factor (NF)-kB activator. The method of the invention is used  
 CC to identify compounds which modulate BCMA activity (and thus NF-kB  
 CC activity). The specification describes a method of identifying a  
 CC polypeptide which increases gene expression from a promoter. The method  
 CC involves contacting a library of with a cell which expresses a  
 CC recombinant anti-cell death gene and a reporter gene operably linked to  
 CC the promoter, and then determining whether the expression of the reporter  
 CC gene is altered as a result of contact with library. The method is useful  
 CC for identifying polypeptides which increase or decrease gene expression  
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for  
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,  
 CC viral infections, inflammatory response, such as rheumatoid arthritis,  
 CC inflammatory bowel disease or septic shock. BCMA is useful for  
 CC identifying compounds that modulate NF-kB expression and thus for drug



CC designing  
XX  
SQ Sequence 185 AA;  
Query Match 67.7%; Score 136; DB 3; Length 185;  
Best Local Similarity 70.6%; Pred. No. 3e-09;  
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;  
QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCQRYC 34  
| : ||||| ||||| ||||| : ||||| ||  
Db 5 CFHSEYFDSLHACKPCHLRCNS--PPATCQPYC 36  
RESULT 51  
AA15490  
ID AAE15490 standard; protein; 185 AA.  
XX  
AC AAE15490;  
XX  
DT 28-MAR-2001 (first entry)  
XX  
DE Murine B cell maturation factor (BCMA) protein.  
XX  
KW Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;  
KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;  
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;  
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;  
KW haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;  
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;  
KW post-streptococcal glomerulonephritis; polyarteritis nodosa.  
XX  
OS Mus musculus.  
XX  
PN WO200068378-A1.  
XX  
PD 16-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US012266.  
XX  
PR 06-MAY-1999; 99US-0132892P.  
PR 01-MAY-2000; 2000US-0201012P.  
XX  
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.  
XX  
PI Shu HS;  
XX  
DR WPI; 2001-016094/02.  
DR N-PSDB; AAD02130.  
XX  
PT Isolated TALL-1 protein is used to identify compounds that regulate B  
PT lymphocyte proliferation, used to treat B lymphocyte associated  
PT autoimmune disorders.  
XX  
PS Claim 37; Page 107-108; 112pp; English.  
XX  
CC The present invention relates to Tumour necrosis factor (TNF) and Apol-  
CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,  
CC proteins (including homologues), and their antibodies. The invention in  
CC particular relates to methods for regulating the interaction between TALL  
CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to  
CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.  
CC TALL-1 protein is useful for identifying compounds that regulate B  
CC lymphocyte proliferation. It is also useful for treating B lymphocyte  
CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus  
CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple  
CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,  
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal  
CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its  
CC corresponding nucleic acid sequence are also useful in diagnostic assays.  
CC The present sequence is a murine B cell maturation factor (BCMA). BCMA is  
CC the receptor for TALL-1 protein

XX  
SQ Sequence 185 AA;  
Query Match 67.7%; Score 136; DB 4; Length 185;  
Best Local Similarity 70.6%; Pred. No. 3e-09;  
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;  
QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCQRYC 34  
| : ||||| ||||| ||||| : ||||| ||  
Db 5 CFHSEYFDSLHACKPCHLRCNS--PPATCQPYC 36  
RESULT 52  
AAE15490  
ID AAE15490 standard; protein; 185 AA.  
XX  
AC AAE15490;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Mouse B cell maturation (BCMA) protein.  
XX  
KW Mouse; transmembrane activator and intracellular CAML interactor; TACI;  
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX  
OS Mus sp.  
XX  
PN WO200187979-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Theill LE, Yu G;  
XX  
DR WPI; 2002-065686/09.  
XX  
PT Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 11; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer

CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is mouse BCMA protein  
XX  
SQ Sequence 185 AA;  
  
Query Match 67.7%; Score 136; DB 5; Length 185;  
Best Local Similarity 70.6%; Pred. No. 3e-09;  
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34  
|:|||||:|||||:|||||:|||||:  
Db 5 CFHSEYFDSLHACKCHLRCSN--PPATCQPYC 36  
  
RESULT 53  
ADZ67762  
ID ADZ67762 standard; protein; 185 AA.  
XX  
AC ADZ67762;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Mouse tumor necrosis factor receptor BCMA.  
XX  
KW Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;  
KW cytostatic.  
XX  
OS Mus musculus.  
XX  
PN WO2005037865-A2.  
XX  
PD 28-APR-2005.  
XX  
PF 18-OCT-2004; 2004WO-US034375.  
XX  
PR 16-OCT-2003; 2003US-0511698P.  
PR 18-OCT-2004; 2004US-0619552P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;  
XX  
DR WPI; 2005-315682/32.  
XX  
PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
PT detecting ligands, and for modulating tumor growth, metastasis and  
PT immunity, such as separating resting from stimulated immune cells.  
XX  
PS Disclosure; SEQ ID NO 10; 132pp; English.  
XX  
CC The invention provides novel tumor necrosis factor receptor ztnfr14  
CC polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors  
CC and antibodies. Human ztnfr14 polynucleotides are used in claimed methods  
CC for detecting a genetic abnormality in a patient and for detecting a  
CC cancer in a patient. Recombinant ztnfr14 polypeptide, optionally  
CC conjugated to a toxin, is used in a claimed method of killing cancer  
CC cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and  
CC antagonists. The polypeptides, polynucleotides and antibodies may also be  
CC used in methods that modulate tumor growth, metastasis, and immunity such  
CC as separating resting from stimulated immune cells. The present sequence  
CC is that of murine TNFR BCMA. This sequence was compared with that of  
CC murine ztnfr14 ADZ67756 in the identification of ztnfr14 as a member of  
CC the TNFR family.  
XX  
SQ Sequence 185 AA;  
  
Query Match 67.7%; Score 136; DB 9; Length 185;  
Best Local Similarity 70.6%; Pred. No. 3e-09;  
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34  
|:|||||:|||||:|||||:|||||:  
Db 5 CFHSEYFDSLHACKCHLRCSN--PPATCQPYC 36

RESULT 54  
AAE15489  
ID AAE15489 standard; protein; 281 AA.  
XX  
AC AAE15489;  
XX  
DT 29-AUG-2003 (revised)  
DT 12-MAR-2002 (first entry)  
XX  
DE Mouse BCMA-human immunoglobulin Fc region fusion protein.  
XX  
KW Human; transmembrane activator and intracellular CAML interactor; TAC1;  
KW cytostatic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
PN WO200187979-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Theill LE, Yu G;  
XX  
DR WPI; 2002-066686/09.  
XX  
PT Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10B; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TAC1 (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.  
XX  
SQ Sequence 281 AA;  
  
Query Match 67.7%; Score 136; DB 5; Length 281;

Best Local Similarity 70.6%; Pred. No. 4.6e-09;		Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;	
Qy	1 CSQNEYFDSLHACIPQLRCSNTPPLTCQRYC 34		
Db	5 CFHSEYFDSLHACKPCHLRCN--PPATCQPYC 36		
RESULT 55			
ID	ABJ38417	standard; protein; 42 AA.	
XX	AC	ABJ38417;	
XX	DT	12-JUN-2003 (first entry)	
XX	DE	TALL-1 related protein SEQ ID No 197.	
XX	KW	TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;	
XX	KW	systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;	
XX	KW	inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;	
XX	KW	Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;	
XX	KW	glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;	
XX	KW	multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;	
XX	KW	gene therapy.	
XX	OS	Homo sapiens.	
XX	PN	WO200292620-A2.	
XX	PD	21-NOV-2002.	
XX	PF	13-MAY-2002; 2002WO-US015273.	
XX	PR	11-MAY-2001; 2001US-0230196P.	
XX	PA	(AMGE-) AMGEN INC.	
XX	PI	Min H, Hsu H;	
XX	WPI	2003-156719/15.	
XX	PT	New TALL-1-binding polypeptide, useful for modulating the activity of	
XX	PT	TALL-1 and in treating, preventing or diagnosing a B-cell-mediated	
XX	PT	autoimmune diseases, cancers or lymphomas.	
XX	PS	Disclosure; Page 26; 236pp; English.	
XX	CC	The invention relates to a novel TALL-1-binding polypeptide comprising a	
XX	CC	defined sequence in the specification. The composition is useful in	
XX	CC	modulating the activity of TALL-1, and in treating, preventing,	
XX	CC	ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune	
XX	CC	disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or	
XX	CC	lymphoma. The composition may also be used in treating inflammations	
XX	CC	(e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,	
XX	CC	asthma, atherosclerosis, cachexia, cirrhosis, diabetes,	
XX	CC	glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple	
XX	CC	myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis	
XX	CC	and vasculitis. Disorders may be treated with the novel composition using	
XX	CC	gene therapy. This sequence represents a TALL-1 related protein of the	
XX	CC	invention	
XX	CC	Sequence 42 AA;	
XX	CC	Query Match 61.7%; Score 124; DB 6; Length 42;	
XX	CC	Best Local Similarity 100.0%; Pred. No. 2.3e-08;	
XX	CC	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 CSQNEYFDSLHACIPQLRRC 21		
Db	22 CSQNEYFDSLHACIPQLRC 42		



**Qy** 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRVC 34  
| : : | : : | : : | : : | : :  
**Db** 6 CPKDOYWDSSRKSCVSCALTCQRS-ORTCTDFC 38

XX  
DE  
XX  
Tumor necrosis factor receptor superfamily member 13b protein, SEQ: 54.  
XX



PT e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.

XX Claim 2; SEQ ID NO 4; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.

XX Sequence 2240 AA;

Query Match 34.1%; Score 68.5; DB 8; Length 2240;  
 Best Local Similarity 45.2%; Pred. No. 15;  
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQ 31  
 Db 1161 CSQDEYFDHEGVCVPCM-----PPTTPQ 1184

RESULT 64

ADRI8913

ID ADR18913 standard; protein; 2258 AA.

XX AC ADR18913;

XX 04-NOV-2004 (first entry)

XX Human mucin-like protein, SCS0004, variant SEQ ID 3.

XX Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;  
 KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;  
 KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;  
 KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;  
 KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;  
 KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;  
 KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX Homo sapiens.

XX Location/Qualifiers

Key 1..18  
 Peptide /label= Signal\_peptide  
 Protein 19..2258  
 /label= Mature\_protein

XX WO2004069136-A2.

XX 19-AUG-2004.

XX 04-FEB-2004; 2004WO-EP050082.

XX 05-FEB-2003; 2003US-0445217P.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Bienkowska J, Mcallister G;

XX WPI; 2004-604324/58.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,  
 PT e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.

PS Claim 2; SEQ ID NO 3; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.

XX Sequence 2258 AA;

Query Match 34.1%; Score 68.5; DB 8; Length 2258;  
 Best Local Similarity 45.2%; Pred. No. 15;  
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQ 31  
 Db 1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202

RESULT 65

ADRI8915

ID ADR18915 standard; protein; 2264 AA.

XX AC ADR18915;

XX 04-NOV-2004 (first entry)

XX His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.

XX Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;  
 KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;  
 KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;  
 KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;  
 KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;  
 KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;  
 KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX Homo sapiens.

XX WO2004069136-A2.

XX 19-AUG-2004.

XX 04-FEB-2004; 2004WO-EP050082.

XX 05-FEB-2003; 2003US-0445217P.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Bienkowska J, Mcallister G;

XX WPI; 2004-604324/58.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,  
 PT e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.

XX Claim 2; SEQ ID NO 5; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small





SQ Sequence 1877 AA;  
Query Match 33.6%; Score 67.5; DB 7; Length 1877;  
Best Local Similarity 37.8%; Pred. No. 17;  
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;  
QY 1 CSQNEVFDLSLLHACIPQCLRCSSNTTP-----LTCOR 32  
DB 1481 CAAVEWDEGSHRCQPCCHKKCSRSGPSEDCQYTCPR 1517  
RESULT 68  
AAE15495  
ID AAE15495 standard; peptide; 33 AA.  
XX AC AAE15495;  
DT 12-MAR-2002 (first entry)  
XX DE Human TACI cysteine-rich consensus region #1.  
XX KW Human; transmembrane activator and intracellular CMLL interactor; TACI;  
KW cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX OS Homo sapiens.  
XX PN WO200187979-A2.  
XX PD 22-NOV-2001.  
XX PF 14-MAY-2001; 2001WO-US015567.  
XX PR 12-MAY-2000; 2000US-0204039P.  
XX PR 27-JUN-2000; 2000US-0214591P.  
XX PR 14-MAY-2001; 2001US-00214591.  
XX PA (AMGE-) AMGEN INC.  
XX PI Theill LE, Yu G;  
XX WPI; 2002-066686/09.  
XX PT Inhibiting activity of B cell maturation protein and/or transmembrane  
activator and intracellular cyclophilin ligand interactor, by  
administering a binding partner for APRIL, a tumor necrosis factor family  
ligand.  
XX PS Claim 1; Fig 12B; 94pp; English.  
XX CC The invention relates to a method for inhibiting TACI (transmembrane  
activator and intracellular CMLL interactor) and/or B cell maturation  
protein (BCMA) activity in a mammal. The method comprises administering a  
specific binding partner for APRIL (G70, a tumor necrosis factor-TNF  
family ligand), having the consensus region of TACI, BCMA, or the TACI/  
BCMA extracellular consensus sequence, but not the extracellular region  
of TACI or BCMA. The method is useful for inhibiting activity of TACI  
and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
lymphoproliferative disorders, one or more solid tumours such as lung,  
gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
antagonists are useful for treating inflammation and immune function  
diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
disease), drug and insect sting allergy, inflammatory bowel disease  
(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
with leucocyte infiltration of the skin or organs. The present sequence

CC is human TACI cysteine-rich consensus region  
XX SQ Sequence 33 AA;  
Query Match 33.1%; Score 66.5; DB 5; Length 33;  
Best Local Similarity 32.4%; Pred. No. 0.39;  
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;  
QY 1 CSQNEVFDLSLLHACIPQCLRCSSNTTPPLTTCORYC 34  
DB 1 CPBEQWDPDLTGCMCKTICNHQS-QRTCAAF 33  
RESULT 69  
ADA49368  
ID ADA49368 standard; peptide; 33 AA.  
XX AC ADA49368;  
XX DT 20-NOV-2003 (first entry)  
XX DE Human TACII cysteine rich domain.  
XX KW TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;  
KW antiarthritic; dermatological; antidiabetic; neuroprotective;  
KW antithyroid; antipyretic; nephrotropic; vasotropic; vaccine;  
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;  
KW insulin dependent diabetes mellitus; multiple sclerosis;  
KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;  
KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;  
KW pemphigus vulgaris; acute rheumatic fever;  
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; TACII; CRD;  
KW cysteine rich domain.  
XX OS Homo sapiens.  
XX PN WO2003035846-A2.  
XX PD 01-MAY-2003.  
XX PF 24-OCT-2002; 2002WO-US034376.  
XX PR 24-OCT-2001; 2001US-0345106P.  
XX PR 14-JAN-2002; 2002US-0348962P.  
XX PR 07-FEB-2002; 2002US-0354966P.  
XX PR 13-AUG-2002; 2002US-0403364P.  
XX PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.  
XX PI Zhang G, Shu H, Liu Y, Xu L;  
XX WPI; 2003-403345/38.  
XX PT Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological  
activity in mammal, has a modification in the region connecting beta  
strands D and E that reduces the biological activity of TALL-1  
antagonist.  
XX PS Disclosure; Page 617; 618pp; English.  
XX CC The invention relates to a novel TALL-1 antagonist protein, comprising a  
sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID  
NO:2, by at least one modification in the region connecting sbgr; strands  
D and E that reduces the biological activity of the TALL-1 antagonist as  
compared to wild-type TALL-1. A protein of the invention has  
immunosuppressive, antirheumatic, neuroprotective, antithyroid, antipyretic,  
dermatological, antidiabetic, neuroprotective, antiinflammatory, antiarthritic,  
nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in  
biological activity in a mammal. TC is useful for treating autoimmune  
diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin  
dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,  
Grave's disease, autoimmune hemolytic anaemia, autoimmune

CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,  
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and  
 CC polyarthritis nodosa. The present sequence represents a cysteine rich  
 CC domain (CRD) module of human TAC11.  
 XX  
 SQ Sequence 33 AA;  
 Query Match 33.1%; Score 66.5; DB 6; Length 33;  
 Best Local Similarity 32.4%; Pred. No. 0.39;  
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 CSQNEVFDLSLHACIPCOLRCSSNTPTPLTCORVC 34  
 Db 1 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 33  
 RESULT 70  
 AAU10951  
 ID AAU10951 standard; protein; 37 AA.  
 XX  
 AC AAU10951;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human AGP-3 receptor cysteine rich repeat region #1.  
 XX  
 KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;  
 KW antidiabetic; analgesic; nephroretropic; osteopathic; cyostatic; fever;  
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;  
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;  
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;  
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;  
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;  
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;  
 KW multiple sclerosis; Parkinson's disease; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185782-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 12-FEB-2001; 2001WO-US004568.  
 XX  
 PR 11-FEB-2000; 2000US-0181800P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2002-049441/06.  
 XX  
 PT Composition, useful for identifying modulator of receptor for treating  
 PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor  
 PT ligand family member) receptor and encoding nucleic acids.  
 XX  
 PS Claim 1; Fig 18; 124pp; English.  
 XX  
 CC The invention relates to a composition (I) comprising AGP-3 receptor  
 CC (tumour necrosis factor ligand family member) related protein (II)  
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related  
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in  
 CC assays to identify cells and tissues that express AGP-3R or proteins  
 CC related to AGP-3R-related protein and for identifying compounds (agonists  
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful  
 CC for identifying intracellular proteins that interact with the respective  
 CC cytoplasmic domains by yeast two-hybrid screening processes. (II) is  
 CC involved in B cell growth, survival and activation particularly in lymph  
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists  
 CC identified using (II) are used for modulating B cell response and are  
 CC used to treat diseases characterised by inflammatory processes or  
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-

CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the  
 CC production of hybridoma cells which are derived from B cells, which  
 CC involves treating the hybridoma cells with (II). (II) is useful in the  
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid  
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are  
 CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis  
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,  
 CC diabetes, fever, glomerulonephritis, inflammatory bowel disease, multiple  
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple  
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,  
 CC septic shock, etc. The nucleic acids are also useful for developing the  
 CC transgenic animals expressing (II), which are useful for producing the  
 CC polypeptides and for the study of in vivo biological activity. The  
 CC present sequence represents the amino acid sequence of human AGP-3  
 CC cysteine-rich repeat region #1  
 XX  
 SQ Sequence 37 AA;  
 Query Match 33.1%; Score 66.5; DB 5; Length 37;  
 Best Local Similarity 32.4%; Pred. No. 0.44;  
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 CSQNEVFDLSLHACIPCOLRCSSNTPTPLTCORVC 34  
 Db 2 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 34  
 RESULT 71  
 ADZ67772  
 ID ADZ67772 standard; protein; 48 AA.  
 XX  
 AC ADZ67772;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Human tumor necrosis factor receptor TAC1 Cys-rich domain.  
 XX  
 KW Tumor necrosis factor receptor; TAC1; cancer; neoplasm; diagnosis;  
 KW cyostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005037865-A2.  
 XX  
 PD 28-APR-2005.  
 XX  
 PF 18-OCT-2004; 2004WO-US034375.  
 XX  
 PR 16-OCT-2003; 2003US-0511698P.  
 PR 18-OCT-2004; 2004US-0619552P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;  
 XX  
 DR WPI; 2005-315682/32.  
 XX  
 PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
 PT detecting ligands, and for modulating tumor growth, metastasis and  
 PT immunity, such as separating resting from stimulated immune cells.  
 XX  
 PS Disclosure; SEQ ID NO 20; 132pp; English.  
 XX  
 CC The invention provides novel tumor necrosis factor receptor (TNFR)  
 CC ztnfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression  
 CC vectors and antibodies. Ztnfr14 polynucleotides are used in claimed  
 CC methods for detecting a genetic abnormality in a patient and for  
 CC detecting a cancer in a patient. Recombinant ztnfr14 polypeptide.  
 CC optionally conjugated to a toxin, is used in a claimed method of killing  
 CC cancer cells. Ztnfr14 polypeptides can be used to detect ligands,  
 CC agonists and antagonists. The polypeptides, polynucleotides and  
 CC antibodies may also be used in methods that modulate tumor growth,  
 CC metastasis, and immunity such as separating resting from stimulated







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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:57:04 ; Search time 18.8 Seconds  
(without alignments)  
174.009 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41  
Perfect score: 201  
Sequence: 1 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	184	2 S43486	B-cell maturation
2	67.5	33.6	1548	2 S34583	serine proteinase
3	64.5	32.1	5376	2 T42215	zonadhesin - mouse
4	61	30.3	1101	2 T16840	hypothetical prote
5	59	29.4	758	2 T15577	hypothetical prote
6	58	28.9	1299	2 T43251	furin (EC 3.4.21.7
7	57.5	28.6	63	2 S07127	chymotrypsin/elast
8	57.5	28.6	1680	2 A43434	furin (EC 3.4.21.7
9	57	28.4	1717	1 A45558	epidermal growth f
10	56	27.9	2476	2 T34022	zonadhesin - pig
11	55.5	27.6	989	2 T01519	hypothetical prote
12	55	27.4	330	2 T25169	hypothetical prote
13	55	27.4	1513	2 T23681	hypothetical prote
14	54.5	27.1	2155	2 T30197	alpha tectorin - m
15	54	26.9	1980	2 S54307	myosin heavy chain
16	54	26.9	2022	2 A59256	myosin-IXb leimila
17	53.5	26.6	758	2 S46625	finger protein xVL
18	53	26.4	1574	2 T13954	MEGF6 protein - ra
19	53	26.4	2824	2 T22759	hypothetical prote
20	52.5	26.1	118	2 S61051	hypothetical prote
21	52	25.9	255	2 A84544	hypothetical prote
22	52	25.9	294	2 T23682	hypothetical prote
23	52	25.9	547	2 T34318	hypothetical prote
24	52	25.9	1474	2 D88550	protein ZC84.6 [im
25	52	25.9	2844	2 S28291	hypothetical prote
26	51.5	25.6	63	2 S57816	antimicrobial pept
27	51.5	25.6	282	2 I48763	siach-1A protein -
28	51.5	25.6	282	2 S35754	siach-1B protein -
29	51.5	25.6	497	2 T27827	hypothetical prote

hypothetical prote  
hypothetical prote  
hypothetical prote  
alpha tectorin - c  
probable transcrip  
hypothetical prote  
hypothetical prote  
cab-binding protei  
chymotrypsin/elast  
ubiquitin / riboso  
hypothetical prote  
probable aminotran  
tumor necrosis fac  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable two-compo  
hypothetical prote  
resistance protein  
hypothetical prote  
hypothetical prote  
homeotic protein m  
hypothetical prote  
paired-box-contain  
protein Tf9.18 [i  
tumor necrosis fac  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable vitellog  
notch-1 protein -  
laminin alpha 5 ch  
hypothetical prote  
serum albumin 1 pr  
serum albumin 2 pr  
hypothetical prote  
seven-pass transme  
trypsin inhibitor  
protein C10G8.4 [i  
tissue factor path  
hypothetical prote  
protein kinase [EC  
protein apx-1 [imp  
CIP synthase (EC 6  
protein C18H9.7 [i  
adenosylhomocyste  
hypothetical prote  
hypothetical prote  
brefeldin A-sensit  
protein MEDEA [imp  
subtilisin-like pr  
subtilisin-like pr  
mucin - rat  
gag-Rail-env poly  
Motch B protein -  
laminin beta-2 cha  
hypothetical prote  
hypothetical prote  
gamma-1-microglu  
probable membrane  
furin (EC 3.4.21.7  
protein F14N23.5 [i  
laminin beta-2 cha  
hypothetical prote  
protein T22A3.8 [i  
hypothetical prote  
hypothetical prote  
laminin alpha chai  
hypothetical 11.7K  
hypothetical prote

103	47	23.4	348	2	T28623	hypothetical prote	176	45	22.4	102	2	S26409	protein 108 precur
104	47	23.4	349	2	D36858	gene G4R protein -	177	45	22.4	104	2	G71202	hypothetical prote
105	47	23.4	349	2	D72175	G2R protein - vari	178	45	22.4	182	2	T28390	ORF MSV229 leucine
106	47	23.4	601	2	C89451	protein T04G9.6 [i	179	45	22.4	187	2	G87521	HNH endonuclease f
107	47	23.4	664	2	AD1136	NADH flavin oxidor	180	45	22.4	320	1	A39479	hemotetic protein m
108	47	23.4	664	2	AD1494	NADH flavin oxidor	181	45	22.4	324	2	T24819	hypothetical prote
109	47	23.4	701	2	S62460	hypothetical prote	182	45	22.4	364	2	JC4249	recF protein - Azo
110	47	23.4	877	2	T41794	RNA polymerase LEF	183	45	22.4	370	2	T37282	probable cathepsin
111	47	23.4	932	2	I52527	FACE4A - mouse (fr	184	45	22.4	384	2	S25771	gas1 protein - mou
112	47	23.4	937	2	I53282	gene FACE4 protein	185	45	22.4	396	2	S53325	tissue factor path
113	47	23.4	1650	2	S53457	dominant autoantig	186	45	22.4	420	2	T30507	probable alkaline
114	47	23.4	2616	2	A57096	model protein prec	187	45	22.4	431	2	G75305	hypothetical prote
115	47	23.4	4660	2	T42737	gp330 protein prec	188	45	22.4	450	2	B97297	hydrogenase chain
116	47	23.4	4733	1	A47437	LDL-receptor-relat	189	45	22.4	464	2	T24011	hypothetical prote
117	46.5	23.1	63	1	T1NBE2	proteinase inhibit	190	45	22.4	479	2	AF2146	deoxyribopyrimidin
118	46.5	23.1	135	2	AD2688	transcription regu	191	45	22.4	511	2	JC7682	spermatogenesis as
119	46.5	23.1	135	2	G97469	hypothetical prote	192	45	22.4	557	2	A48434	variant-specific s
120	46.5	23.1	186	2	A45910	ultra-high-sulfur	193	45	22.4	661	2	G97717	hypothetical prote
121	46.5	23.1	202	2	T22327	hypothetical prote	194	45	22.4	672	2	G71719	hypothetical prote
122	46.5	23.1	233	2	T34078	hypothetical prote	195	45	22.4	702	2	T21148	hypothetical prote
123	46.5	23.1	278	2	T05774	hypothetical prote	196	45	22.4	763	2	S51300	probable membrane
124	46.5	23.1	389	2	T29488	hypothetical prote	197	45	22.4	964	2	T30455	hypothetical prote
125	46.5	23.1	413	2	G82422	anaerobic glycerol	198	45	22.4	1397	2	T46354	hypothetical prote
126	46.5	23.1	419	2	S69207	vascular endotheli	199	45	22.4	1839	1	RWPEM	genome polyprotein
127	46.5	23.1	425	2	T18592	hypothetical prote	200	45	22.4	2548	2	E59435	myosin IXA [import
128	46.5	23.1	461	2	B88953	protein F16B4.8 [i	201	45	22.4	2626	2	T31099	myosin-RhoGAP prot
129	46.5	23.1	461	2	T32863	hypothetical prote	202	45	22.4	2626	2	A53102	alpha-2-macroglobu
130	46.5	23.1	600	2	T18593	hypothetical prote	203	45	22.4	4544	1	S02392	alpha-2-macroglobu
131	46.5	23.1	802	2	T24293	hypothetical prote	204	45	22.4	4545	1	S25111	MHC class II beta
132	46.5	23.1	874	2	JQ0983	genome polyprotein	205	44.5	22.1	142	2	IS1063	high-sulfur kerati
133	46.5	23.1	949	2	T24294	hypothetical prote	206	44.5	22.1	175	2	S37649	genome polyprotein
134	46.5	23.1	1124	1	I58388	protein-tyrosine k	207	44.5	22.1	180	2	PC1305	MHC class II beta
135	46.5	23.1	1365	2	S14871	suppressor two of	208	44.5	22.1	217	2	IS1062	hypothetical prote
136	46.5	23.1	1597	2	S68420	citron - mouse	209	44.5	22.1	251	2	S23821	hypothetical prote
137	46.5	23.1	1935	2	T39411	RNA helicase - fis	210	44.5	22.1	263	1	ASLJFP	vif protein - feli
138	46.5	23.1	2111	2	T15390	hypothetical prote	211	44.5	22.1	298	2	E95532	conserved hypotet
139	46.5	23.1	3033	1	GNWJ78	genome polyprotein	212	44.5	22.1	347	2	AC0825	anaerobic sulfate
140	46	22.9	99	2	S60231	gibberellin-regula	213	44.5	22.1	357	2	T21152	hypothetical prote
141	46	22.9	232	2	A40738	hypothetical prote	214	44.5	22.1	368	2	H81059	phosphoserine amin
142	46	22.9	311	2	B64332	hypothetical prote	215	44.5	22.1	396	1	JH0633	cellular tumor ant
143	46	22.9	335	2	T12789	interleukin 12 p40	216	44.5	22.1	400	2	F81432	probable transamin
144	46	22.9	366	2	T15925	hypothetical prote	217	44.5	22.1	481	2	A56429	I-kappa-B-related
145	46	22.9	369	2	S21471	genome polyprotein	218	44.5	22.1	493	2	JC5486	membrane glycoprot
146	46	22.9	404	2	C96549	hypothetical prote	219	44.5	22.1	592	1	A30314	protein kinase C (
147	46	22.9	430	2	AB0811	probable transcrip	220	44.5	22.1	592	1	JC1480	protein kinase C (
148	46	22.9	439	2	T32627	hypothetical prote	221	44.5	22.1	597	1	S53711	C4BP alpha chain p
149	46	22.9	440	2	T41766	ARIF-1 orf20/21 -	222	44.5	22.1	654	2	C96782	unknown protein P2
150	46	22.9	458	2	S61974	SSU1 protein - yea	223	44.5	22.1	949	2	S40241	probable membrane
151	46	22.9	528	2	S14944	regulatory protein	224	44.5	22.1	1115	2	S40241	G protein-coupled
152	46	22.9	593	2	I51213	drebrin - chicken	225	44.5	22.1	1126	2	A49208	transmembrane prot
153	46	22.9	782	2	S18031	genome polyprotein	226	44.5	22.1	1171	2	A49216	metabotropic gluta
154	46	22.9	783	2	A41627	furin (EC 3.4.21.7	227	44.5	22.1	1180	2	JC2132	metabotropic gluta
155	46	22.9	876	2	B72856	late expression fa	228	44.5	22.1	1212	2	JC2131	metabotropic gluta
156	46	22.9	1747	2	T43162	vitellogenin - gyp	229	44.5	22.1	1297	2	T52065	probable myb-relat
157	46	22.9	1753	2	T00350	hypothetical prote	230	44.5	22.1	1661	2	T31330	head-activator bin
158	46	22.9	2135	2	T14602	variant-specific s	231	44.5	22.1	1791	2	T02345	hypothetical prote
159	46	22.9	2910	2	T42214	otogelin - mouse	232	44.5	22.1	2150	2	T32497	hypothetical prote
160	46	22.9	3084	1	MMWSA	laminin alpha-1 ch	233	44.5	22.1	2471	2	A49128	cell-fate determin
161	45.5	22.6	131	2	S55380	Norrie disease pro	234	44	21.9	72	2	B27725	small proline-rich
162	45.5	22.6	133	2	A57005	Norrie disease can	235	44	21.9	93	2	JE0159	gibberellin-stimul
163	45.5	22.6	185	2	D82755	conserved hypotet	236	44	21.9	114	2	D75422	hypothetical prote
164	45.5	22.6	201	2	D71190	hypothetical prote	237	44	21.9	118	2	T49515	hypothetical prote
165	45.5	22.6	209	2	A88104	protein W10G11.3 [	238	44	21.9	128	2	T22276	hypothetical prote
166	45.5	22.6	225	2	S57810	hypothetical prote	239	44	21.9	165	2	S74697	hypothetical prote
167	45.5	22.6	318	2	A45522	variant surface gl	240	44	21.9	165	2	AB2113	hypothetical prote
168	45.5	22.6	386	2	A41950	retrovirus-related	241	44	21.9	166	2	H89044	protein B0238.12 [
169	45.5	22.6	392	2	T29519	hypothetical prote	242	44	21.9	167	2	H72579	hypothetical prote
170	45.5	22.6	697	2	E96752	hypothetical prote	243	44	21.9	185	2	A13991	conserved hypotet
171	45.5	22.6	704	2	T50303	hypothetical prote	244	44	21.9	185	2	A95292	hypothetical prote
172	45.5	22.6	749	2	S13518	transposase Tam3 -	245	44	21.9	191	2	B46412	keratin KA5.4 - s
173	45.5	22.6	1077	2	T41146	probable cysteine-	246	44	21.9	199	2	B86288	F9L1.31 protein - s
174	45.5	22.6	1171	2	T13065	PIP82 protein - fr	247	44	21.9	224	2	C81417	probable transcrip
175	45	22.4	99	2	S40012	fill protein - gar	248	44	21.9	242	2	T29699	hypothetical prote



249 44 21.9 304 1 TIHUGK  
250 44 21.9 319 2 B72852  
251 44 21.9 334 2 E44221  
252 44 21.9 338 2 T18715  
253 44 21.9 340 2 S58770  
254 44 21.9 361 2 B48827  
255 44 21.9 405 2 T42992  
256 44 21.9 405 2 T26678  
257 44 21.9 418 2 A64508  
258 44 21.9 441 2 S12707  
259 44 21.9 455 2 E90316  
260 44 21.9 469 2 E86421  
261 44 21.9 502 2 T20130  
262 44 21.9 548 2 T16642  
263 44 21.9 601 2 B36346  
264 44 21.9 659 2 T01520  
265 44 21.9 661 2 B96596  
266 44 21.9 667 2 T01999  
267 44 21.9 669 2 T06702  
268 44 21.9 683 2 C36346  
269 44 21.9 685 2 S78040  
270 44 21.9 705 2 S34968  
271 44 21.9 761 2 H65083  
272 44 21.9 776 2 A82787  
273 44 21.9 780 2 A34102  
274 44 21.9 780 2 T31548  
275 44 21.9 782 2 S19876  
276 44 21.9 838 2 T20125  
277 44 21.9 862 1 QRM5LD  
278 44 21.9 879 2 C90879  
279 44 21.9 879 2 H64888  
280 44 21.9 879 2 G85739  
281 44 21.9 915 1 A48225  
282 44 21.9 1111 2 T26972  
283 44 21.9 1166 1 S06142  
284 44 21.9 1221 2 T23472  
285 44 21.9 1255 1 A24571  
286 44 21.9 3075 2 S14458  
287 43.5 21.6 61 2 S57815  
288 43.5 21.6 155 2 B32669  
289 43.5 21.6 247 2 I51060  
290 43.5 21.6 292 2 B42822  
291 43.5 21.6 312 2 T32379  
292 43.5 21.6 339 1 KHRTB  
293 43.5 21.6 347 2 A38453  
294 43.5 21.6 352 2 S11926  
295 43.5 21.6 356 2 G88968  
296 43.5 21.6 481 2 S62427  
297 43.5 21.6 484 2 JC8020  
298 43.5 21.6 592 2 JN0877  
299 43.5 21.6 595 2 T39228  
300 43.5 21.6 625 2 T37604

ALIGNMENTS

RESULT 1  
B-cell maturation factor - human  
N:Alternate names: BCM protein; BCMA protein; BEL protein  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S43486; S31208; S36661  
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
Nucleic Acids Res. 22, 1147-1154, 1994  
A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire  
A:Reference number: S43486; MUID:94218235; PMID:8165126  
A:Accession: S43486  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-184 <LAA>  
A:Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:9471244; PID

R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
EMBO J. 11, 3897-3904, 1992  
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)  
A:Reference number: S31208; MUID:93010984; PMID:1396583  
A:Accession: S31208  
A:Molecule type: mRNA  
A:Residues: 1-184 <LAA>  
A:Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID  
A:Accession: S36661  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 4-184 <LAA>  
A:Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955  
C:Genetics:  
A:Gene: GDB:BCMA  
A:Cross-references: GDB:135977; OMIM:109545  
A:Map position: 16p13.1-16p13.1  
A:Introns: 44/1; 93/1  
C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 201; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 41

RESULT 2  
S34583  
serine proteinase (EC 3.4.21.-) PC6B - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Dec-1993 #sequence revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S34583  
R:Nakagawa, T.; Murakami, K.; Nakayama, K.  
FEBS Lett. 327, 165-171, 1993  
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a  
A:Reference number: S34583; MUID:93327934; PMID:8335106  
A:Accession: S34583  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1548 <NAK>  
A:Cross-references: UNIPROT:Q04592; UNIPARC:UPI000016CF9E; GB:D17583; NID:9407344; PIDN:FI  
C:Keywords: hydrolase; serine proteinase

Query Match 33.6%; Score 67.5; DB 2; Length 1548;  
Best Local Similarity 37.8%; Pred. No. 2.4;  
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;  
Qy 1 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 32  
Db 1152 CAAVEYWDGSHRCQCHKKCRSGSPEDQCYTCPR 1188

RESULT 3  
T42215  
zonadhesin - mouse  
N:Alternate names: sperm-specific membrane protein  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T42215  
R:Gao, Z.; Garbers, D.L.  
J. Biol. Chem. 273, 3415-3421, 1998  
A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro  
A:Reference number: Z22080; MUID:98123114; PMID:9452463  
A:Accession: T42215  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5376 <GAO>  
A:Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:93327420; PI  
C:Genetics:  
A:Gene: Zan



A; Cross-references: FlyBase:FBgn0004598  
C; Keywords: hydrolase; serine proteinase; transmembrane protein  
F; 409-652/Domain: subtilisin homology <SBT>  
F; 418, 457, 638/Active site: Asp, His, Ser #status predicted

Query Match 28.6%; Score 57.5; DB 2; Length 1680;  
Best Local Similarity 34.3%; Pred. No. 41;  
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCQLRCS-NTPLPTCQRYC 34  
|||::: : ||| |  
Db 1199 CSESEFYQVEGQCRPCHASCGSCNGPADTSCSTC 1233  
|||::: : ||| |

RESULT 9  
A45558  
N; Contain: epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)  
C; Species: Schistosoma mansoni  
C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C; Accession: A45558; S27836  
R; Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.  
Mol. Biochem. Parasitol. 53, 17-32, 1992  
A; Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep  
A; Reference number: A45558; MUID:92365727; PMID:1501637  
A; Accession: A45558  
A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-1717 <SHO>  
A; Cross-references: UNIPROT:Q26566; UNIPARC:UPI000007DCD7; EMBL:M86396; NID:gl60957; PII  
A; Note: sequence extracted from NCBI backbone (NCBIP:111129)  
C; Genetics:  
A; Gene: SER  
C; Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology  
C; Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein  
F; 1-19/Domain: signal sequence #status predicted <Sig>  
F; 20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>  
F; 1018-1323/Domain: protein kinase homology <KIN>  
F; 1026-1034/Region: protein kinase ATP-binding motif

Query Match 28.4%; Score 57; DB 1; Length 1717;  
Best Local Similarity 40.9%; Pred. No. 48;  
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCQLRCS 22  
|||::: : ||| |  
Db 646 CPRNTYIDPQTRHCLPCNESCS 667  
|||::: : ||| |

RESULT 10  
T34022  
zonadhesin - pig  
C; Species: Sus scrofa domestica (domestic pig)  
C; Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C; Accession: T34022  
R; Hardy, D.M.; Garbers, D.L.  
J. Biol. Chem. 270, 26025-26028, 1995  
A; Title: A sperm membrane protein that binds in a species-specific manner to the egg ext  
A; Reference number: 221464; MUID:96064658; PMID:7592795  
A; Accession: T34022  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: mRNA  
A; Residues: 1-2476 <HAR>  
A; Cross-references: UNIPROT:Q29983; UNIPARC:UPI000013C373; EMBL:U40024; NID:gl066465; P  
A; Experimental source: strain Weishan; testis  
C; Genetics:  
A; Gene: Zan  
C; Function:  
A; Description: may be involved in sperm adhesion to the zona pellucida

Query Match 27.9%; Score 56; DB 2; Length 2476;  
Best Local Similarity 31.6%; Pred. No. 87;  
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

R;Matthews, L.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19781  
A;Accession: T23681  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1513 <WIL>  
A;Cross-references: UNIPROT:O17970; UNIPARC:UPI0000076B6D; EMBL:Z81573; PIDN:CAB04625.1;  
A;Experimental source: clone M02G9  
C;Genetics:  
A;Gene: CESP:M02G9.1  
A;Map position: 2  
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1  
Query Match 27.4%; Score 55; DB 2; Length 1513;  
Best Local Similarity 44.8%; Pred. No. 75;  
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 2;  
QY 8 DSLHAC-IPCQRC-SSNTPPLTCQRC 34  
DB 141 DSCQNVQVCQACVQSNSPPAVCQQT 169  
RESULT 14  
T30197  
alpha tectorin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30197  
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.  
J. Biol. Chem. 272, 8791-8801, 1997  
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com  
A;Reference number: Z20771; MUID:97236843; PMID:9079715  
A;Accession: T30197  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-2155 <LEG>  
A;Cross-references: UNIPROT:O08523; UNIPARC:UPI000002793C; EMBL:X98805; NID:g1915908; PI  
A;Experimental source: strain CDI; whole cochlea  
A;Note: non-collagenous protein only expressed in the inner ear, by cells both in and su  
Query Match 27.1%; Score 54.5; DB 2; Length 2155;  
Best Local Similarity 29.4%; Pred. No. 1.2e+02;  
Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;  
QY 1 CSQNEYFDSLHACIPCQRCSSNTPPLTCQRC 34  
DB 1372 CPPNSHYEVCVQCP---RCAAIRLKSDCNHYC 1402  
RESULT 15  
S54307  
myosin heavy chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S54307  
R;Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.  
EMBO J. 14, 697-704, 1995  
A;Title: A novel type of myosin implicated in signalling by rho family GTPases.  
A;Reference number: S54307; MUID:95188874; PMID:7882973  
A;Accession: S54307  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1980 <REI>  
A;Cross-references: UNIPROT:Q63358; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:g6339998; PI  
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi  
C;Keywords: nucleotide binding; P-loop  
F;149-942/Domain: myosin motor domain homology <MMOT>  
F;239-246/Region: nucleotide-binding motif A (P-loop)  
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>  
Query Match 26.9%; Score 54; DB 2; Length 1980;  
Best Local Similarity 52.9%; Pred. No. 1.2e+02;

Submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19781  
A;Accession: T23681  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1513 <WIL>  
A;Cross-references: UNIPROT:O17970; UNIPARC:UPI0000076B6D; EMBL:Z81573; PIDN:CAB04625.1;  
A;Experimental source: clone M02G9  
C;Genetics:  
A;Gene: CESP:M02G9.1  
A;Map position: 2  
A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1  
Query Match 27.4%; Score 55; DB 2; Length 1513;  
Best Local Similarity 44.8%; Pred. No. 75;  
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 2;  
QY 8 DSLHAC-IPCQRC-SSNTPPLTCQRC 34  
DB 141 DSCQNVQVCQACVQSNSPPAVCQQT 169  
RESULT 14  
T30197  
alpha tectorin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30197  
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.  
J. Biol. Chem. 272, 8791-8801, 1997  
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com  
A;Reference number: Z20771; MUID:97236843; PMID:9079715  
A;Accession: T30197  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-2155 <LEG>  
A;Cross-references: UNIPROT:O08523; UNIPARC:UPI000002793C; EMBL:X98805; NID:g1915908; PI  
A;Experimental source: strain CDI; whole cochlea  
A;Note: non-collagenous protein only expressed in the inner ear, by cells both in and su  
Query Match 27.1%; Score 54.5; DB 2; Length 2155;  
Best Local Similarity 29.4%; Pred. No. 1.2e+02;  
Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;  
QY 1 CSQNEYFDSLHACIPCQRCSSNTPPLTCQRC 34  
DB 1372 CPPNSHYEVCVQCP---RCAAIRLKSDCNHYC 1402  
RESULT 15  
S54307  
myosin heavy chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S54307  
R;Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.  
EMBO J. 14, 697-704, 1995  
A;Title: A novel type of myosin implicated in signalling by rho family GTPases.  
A;Reference number: S54307; MUID:95188874; PMID:7882973  
A;Accession: S54307  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1980 <REI>  
A;Cross-references: UNIPROT:Q63358; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:g6339998; PI  
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi  
C;Keywords: nucleotide binding; P-loop  
F;149-942/Domain: myosin motor domain homology <MMOT>  
F;239-246/Region: nucleotide-binding motif A (P-loop)  
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>  
Query Match 26.9%; Score 54; DB 2; Length 1980;  
Best Local Similarity 52.9%; Pred. No. 1.2e+02;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 16 PCQLRCSSNTPPLTCQR 32  
DB 1812 PCLLRCPDNDSDLTSMK 1828  
RESULT 16  
AS9256  
myosin-IXb [similarity] - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 31-Dec-2004  
C;Accession: AS9256; I61700  
R;Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.  
J. Cell Sci. 109, 653-661, 1996  
A;Title: Human myosin-IXb, an unconventional myosin with a chimera-like rho/rac GTPase-  
A;Reference number: AS9256; MUID:97063843; PMID:8907710  
A;Accession: AS9256  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-2022 <WIR>  
A;Cross-references: UNIPROT:Q14788; UNIPARC:UPI0000161189; GB:U42391; NID:g1147782; PIDN:  
R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.  
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994  
A;Title: Identification and overlapping expression of multiple unconventional myosin gene  
A;Reference number: AS5758; MUID:94294418; PMID:8022818  
A;Accession: I61700  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 234-322 <RES>  
A;Cross-references: UNIPARC:UPI0000073918; GB:L29149; NID:g457257; PIDN:AAA20912.1; PID:9  
C;Genetics:  
A;Gene: GDB:WYO9B; OMIM:602129  
A;Map position: 19p13.1  
C;Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolog  
C;Keywords: nucleotide binding; P-loop  
F;149-941/Domain: myosin motor domain homology #status atypical <MMO>  
F;239-246/Region: nucleotide-binding motif A (P-loop)  
Query Match 26.9%; Score 54; DB 2; Length 2022;  
Best Local Similarity 52.9%; Pred. No. 1.3e+02;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 16 PCQLRCSSNTPPLTCQR 32  
DB 1852 PCLLRCPDNDSDLTSMK 1868  
RESULT 17  
S46625  
finger protein YJL206c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: probable membrane protein YJL206c; protein J0316  
C;Species: Saccharomyces cerevisiae  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Oct-2004  
C;Accession: S46625; S56993  
R;Purnelle, B.; Coster, F.; Goffeau, A.  
Yeast 10, 1235-1249, 1994  
A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies  
ase gene ACO1 and two homologues to chromosome III genes.  
A;Reference number: S46621; MUID:95274326; PMID:7754713  
A;Accession: S46625  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-758 <PUR>  
A;Cross-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:g1183992; PI  
R;Purnelle, B.; Coster, F.; Goffeau, A.  
submitted to the Protein Sequence Database, September 1995  
A;Reference number: S56977  
A;Accession: S56993  
A;Molecule type: DNA  
A;Residues: 1-758 <PUW>  
A;Cross-references: UNIPARC:UPI000013B60A; EMBL:Z49481; NID:g1015584; PIDN:CAA89502.1; PI  
C;Genetics:





Qy 10 LLHACIPQLRCSSNT--PLTTCQRYC 34  
Db 24 MIEACIGNGRGNENVGPPYCCSGFC 49

RESULT 27  
siah-1A protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I48763; S35753  
R:Della, N.G.; Senior, P.V.; Bowtell, D.D.  
Development 117, 1333-1343, 1993  
A:Title: Isolation and characterisation of murine homologues of the Drosophila seven in  
A:Reference number: I48763; MUID:94008536; PMID:8404535  
A:Accession: T27827  
A:Molecule type: DNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-282 <RES>  
A:Cross-references: UNIPROT:P61092; UNIPARC:UPI00000098B3; EMBL:Z19579; NID:G297034; PID  
C:Superfamily: Drosophila developmental protein siah; RING finger homology

Query Match 25.6%; Score 51.5; DB 2; Length 282;  
Best Local Similarity 41.9%; Pred. No. 47;  
Matches 13; Conservative 3; Mismatches 12; Indels 3; Gaps 1;

Qy 7 FDSLHACIPQ---LRCSSNTPLTTCQRYC 34  
Db 45 FDYVLPPLTQCQSHLVCSNCRPKLTCTCPTC 75

RESULT 28  
siah-1B protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: I48764; S35754  
R:Della, N.G.; Senior, P.V.; Bowtell, D.D.  
Development 117, 1333-1343, 1993  
A:Title: Isolation and characterisation of murine homologues of the Drosophila seven in  
A:Reference number: I48763; MUID:94008536; PMID:8404535  
A:Accession: T27827  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-282 <RES>  
A:Cross-references: UNIPROT:O06985; UNIPARC:UPI000002451E; EMBL:Z19580; NID:G297801; PID  
C:Superfamily: Drosophila developmental protein siah; RING finger homology

Query Match 25.6%; Score 51.5; DB 2; Length 282;  
Best Local Similarity 41.9%; Pred. No. 47;  
Matches 13; Conservative 3; Mismatches 12; Indels 3; Gaps 1;

Qy 7 FDSLHACIPQ---LRCSSNTPLTTCQRYC 34  
Db 45 FDYVLPPLTQCQSHLVCSNCRPKLTCTCPTC 75

RESULT 29  
T27827  
hypothetical protein ZK287.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27827  
R:McMurray, A.  
submitted to the EMBL Data Library, April 1996  
A:Reference number: Z20425  
A:Accession: T27827  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-497 <WIL>  
A:Cross-references: UNIPROT:O23460; UNIPARC:UPI000007F2F3; EMBL:Z70757; PIDN:CAA94805.1;  
A:Experimental source: clone ZK287

C:Genetics:  
A:Gene: CESP:ZK287.1  
A:Map position: 5  
A:Introns: 20/1; 44/2; 99/3; 339/3; 443/2

Query Match 25.8%; Score 51.5; DB 2; Length 497;  
Best Local Similarity 38.5%; Pred. No. 77;  
Matches 10; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

Qy 14 CIPCOLRCSSNTPL-----TCQRYC 34  
Db 15 CVASQGRCSADTCTPCVAARKTCDEHC 40

RESULT 30  
T21773  
hypothetical protein T01D3.6b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21773; T24297  
R:Steward, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19470  
A:Accession: T21773  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-915 <WIL>  
A:Cross-references: UNIPROT:O02364; UNIPARC:UPI000002A1C9; EMBL:Z81527; PIDN:CAB04280.1;  
A:Experimental source: clone F35E12  
R:Steward, C.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19870  
A:Accession: T24297  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-915 <W12>  
A:Cross-references: UNIPARC:UPI000002A1C9; EMBL:Z81110; PIDN:CAB03263.1; GSPDB:GN00023.1;  
A:Experimental source: clone T01D3  
C:Genetics:  
A:Gene: CESP:T01D3.6b  
A:Map position: 5  
A:Introns: 38/2; 87/3; 128/2; 242/2; 374/3; 404/3; 722/3; 830/3; 845/1

Query Match 25.6%; Score 51.5; DB 2; Length 915;  
Best Local Similarity 25.5%; Pred. No. 1.3e+02;  
Matches 12; Conservative 3; Mismatches 19; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIP-----COLRCSSNTPLTTCQRYC 34  
Db 456 CTFTYFLQYCOLALPQVANNQWRAQINCPLACPLNHPSTCTSSC 502

RESULT 31  
T21772  
hypothetical protein T01D3.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21772; T24296  
R:Steward, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19470  
A:Accession: T21772  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-927 <WIL>  
A:Cross-references: UNIPROT:O02364; UNIPARC:UPI0000086677; EMBL:Z81527; PIDN:CAB04279.1;  
A:Experimental source: clone F35E12  
R:Steward, C.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19870  
A:Accession: T24296  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA





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C:Species: Ascaris lumbricoides (common roundworm)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S08572
R:Babin, D.R.; Peanaaky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A:Title: The iso inhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the prima
A:Reference number: S07127; MUID:84255715; PMID:6564898
A:Accession: S08572
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <BA>
A:Cross-references: UNIPARC:UP10000176391
C:Superfamily: roundworm trypsin inhibitor

      Query Match      24.9%; Score 50; DB 2; Length 63;
      Best Local Similarity 30.8%; Pred. No. 20;
      Matches 12; Conservative 6; Mismatches 9; Indels 12; Gaps 3;

Qy      1  CSQNEFDLLHACIPCOLRC--SSNTP-----PLTCQ 31
      | : | : | : | : | : | : | : | : | :
Db      4  CGKNEVWTE-----CTGCELCGQDENTPCALWCRRPSC 38

RESULT 39
SI0332
Ubiquitin / ribosomal protein CEP52 - common tobacco (fragment)

```

C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C:Accession: S10332  
R:Genschik, P.; Parmentier, Y.; Criqui, M.C.; Fleck, J.  
Nucleic Acids Res. 18, 4007, 1990  
A:Title: Sequence of a ubiquitin carboxyl extension protein of Nicotiana tabacum.  
A:Reference number: S10332; MUID:90326543; PMID:2165257  
A:Accession: S10332  
A:Molecule type: DNA  
A:Residues: 1-74 <GEN>  
A:Cross-references: UNIPROT:P19379; UNIPARC:UPI00001715C; EMBL:X53011  
C:Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; ubiquitin  
C:Keywords: DNA binding; protein biosynthesis; ribosome; zinc finger  
F:1-3/Product: ubiquitin (fragment) #status predicted <UBI>  
F:3-74/Product: ribosomal protein CEP52 #status predicted <RIB>  
F:3-74/Domain: ribosomal protein CEP52 homology <CPH>  
F:22-61/Region: zinc finger CCCC motif  
F:68-74/Region: nuclear location signal

Query Match	24.9%	Score 50;	DB 2;	Length 74;
Best Local Similarity	44.4%	Pred. No. 23;		
Matches 8; Conservative		2; Mismatches	8; Indels	0; Gaps 0;

QY 14 CIPCOLRCSSNTPPLTQC 31  
DB 22 CRKCYVRCRPTPQRTCR 39

RESULT 40  
T30370  
hypotheoretical protein ORF23 - Lymantria dispar nuclear polyhedrosis virus  
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T30370  
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr,  
Virology 253, 17-34, 1999  
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d  
A:Reference number: Z20836; PMID:9887315  
A:Accession: T30370  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

Query Match 24.9%; Score 50; DB 2; Length 342;  
Best Local Similarity 50.0%; Pred. No. 85;

Query Match 24.9%; Score 50; DB 2; Length 342;  
Best Local Similarity 50.0%; Pred. No. 85;



A:Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
BioSci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from  
A:Reference number: JC2404; MUID:95128033; PMID:7765720  
A:Accession: JC2404  
A:Molecule type: protein  
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A:Cross-references: UNIPARC:UPI00001736E4  
A:Experimental source: urine  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Genetics:  
A:Gene: GDB:TNFR1  
A:Cross-references: GDB:125913; OMIM:191190  
A:Map position: 12p13.2-12p13.2  
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-45/Domain: signal sequence #status predicted <SIG>  
F:22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F:30-211/Domain: extracellular #status predicted <EXT>  
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-196/Domain: NGF receptor repeat homology <NG4>  
F:212-234/Domain: transmembrane #status predicted <MEM>  
F:235-455/Domain: intracellular #status predicted <INT>  
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 24.9%; Score 50; DB 1; Length 455;  
Best Local Similarity 35.3%; Pred. No. 1.1e+02;  
Matches 12; Conservative 5; Mismatches 13; Indels 4; Gaps 2;  
Qy 1 CSQNEYFDSLHACIPCOLRCSS---NTPTTCQY 31  
Db 127 CRKNQRYHWSNLFQCFNCSL-CLNGTVHLSCQ 159  
RESULT 43  
T27318  
hypothetical protein Y69H2.3a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27318  
R;McMurray, A.  
A:Reference number: Z20343  
A:Experimental source: translated from GB/EMBL/DBJ  
A:Accession: T27318  
A:Molecule type: DNA  
A:Residues: 1-561 <WIL>  
A:Cross-references: UNIPROT:Q9UIT6; UNIPARC:UPI0000164288; EMBL:Z98877; PIDN:CAB54472.1;  
A:Experimental source: clone Y69H2  
C:Genetics:  
A:Gene: CESP:Y69H2.3a  
A:Map position: 5  
A:Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3  
Query Match 24.9%; Score 50; DB 2; Length 561;  
Best Local Similarity 32.4%; Pred. No. 1.3e+02;  
Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;  
Qy 1 CSQNEYFDSLHACIPCOLRCSS---NTPTTCQY 34  
Db 499 CRSNEKFE-----PKTVCSDTKCNEPRFCPCQVC 528  
RESULT 44  
T27319  
hypothetical protein Y69H2.3b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T27319  
R;McMurray, A.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z20343  
A:Accession: T27319  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-626 <WIL>  
A:Cross-references: UNIPROT:Q9UIT5; UNIPARC:UPI0000164289; EMBL:Z98877; PIDN:CAB54473.1;  
A:Experimental source: clone Y69H2  
C:Genetics:  
A:Gene: CESP:Y69H2.3b  
A:Map position: 5  
A:Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2; 586/3  
Query Match 24.9%; Score 50; DB 2; Length 626;  
Best Local Similarity 32.4%; Pred. No. 1.4e+02;  
Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;  
Qy 1 CSQNEYFDSLHACIPCOLRCSS---NTPTTCQY 34  
Db 564 CRSNEKFE-----PKTVCSDTKCNEPRFCPCQVC 593  
RESULT 45  
T23573  
hypothetical protein K10D3.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T23573  
R;McMurray, A.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19762  
A:Accession: T23573  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-922 <WIL>  
A:Cross-references: UNIPROT:Q21418; UNIPARC:UPI00000762C2; EMBL:Z75545; PIDN:CAA9986.1;  
A:Experimental source: clone K10D3  
C:Genetics:  
A:Gene: CESP:K10D3.4  
A:Map position: 1  
A:Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2  
Query Match 24.9%; Score 50; DB 2; Length 922;  
Best Local Similarity 29.3%; Pred. No. 2e+02;  
Matches 12; Conservative 7; Mismatches 14; Indels 8; Gaps 2;  
Qy 1 CSQNEYFDSLHA--CIPCOLRCSSNTTP-----LTCQRY 33  
Db 68 CTQNRQCEAVPGAYCHSGECRCANNQPPFTRDGLVCLNV 108  
RESULT 46  
F96596  
hypothetical protein TSA14.15 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: F96596  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: F96596  
A:Status: preliminary  
A:Molecule type: DNA

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A;Residues: 1-1360 <STO>
A;Cross-references: UNIPROT_Q9ZVU3; UNIPARC:UIP000009D265; GB:AEO05173; NID:g4204269; PID:
C;Genetics:
A;Gene: TSA14.15
A;Map position: 1

Query Match      24.8%   Score 50; DB 2; Length 1360;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches    8; Conservative          4; Mismatches     4; Indels       0; Gaps      0;

Qy      4 NEYFDSLHACIPCQL 19
        | : |||||
Db      947 NKUTDDLVYACLPSL 962

RESULT 47
G83398
probable two-component sensor PAI979 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83398
R;Slover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83398
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-216 <STO>
A;Cross-references: UNIPROT_Q912C8; UNIPARC:UIP00000C553D; GB:AEO04624; GB:AEO04091; NID:
C;Genetics:
A;Gene: PAI979

Query Match      24.6%   Score 49.5; DB 2; Length 216;
Best Local Similarity 34.3%; Pred. No. 66;
Matches    12; Conservative         2; Mismatches    12; Indels     9; Gaps      1;

Qy      3 QNEYFDLSLHAC-----IPCQLRCSSNTPL 28
        | : |||||
Db      86 QRSLDEALRACVADWQGQGIACELRGGLPLPL 120

RESULT 48
T27303
hypothetical protein Y68A4A.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27303
R;Steward, C.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20340
A;Accession: T27303
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-392 <WIL>
A;Cross-references: UNIPROT_Q9XXP6; UNIPARC:UIP000007EED1; EMBL.AL021503; PIDN:CAA16424.
C;Genetics:
A;Gene: CSP.Y68A4A.10
A;Map position: 5
A;Introns: 45/2; 74/3; 139/3; 175/2; 190/3; 241/3; 305/3; 356/3

Query Match      24.6%   Score 49.5; DB 2; Length 392;
Best Local Similarity 40.9%; Pred. No. 1.1e+02;
Matches     9; Conservative         6; Mismatches     6; Indels     1; Gaps      1;

Qy      13 ACIPCQLRCSSNTPLPTCYRYC 34
        |:||| |::|
Db     189 SCLPCQ-TCASFDPMSKATC 209

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C;Species: Saccharomyces cerevisiae  
C;Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
A;Accession: S30015; S37821  
R;Pascolo, S.; Ghazvini, M.; Boyer, J.; Collea, L.; Thierry, A.; Dujon, B.  
Yeast 8, 987-995, 1992  
A;Title: The sequence of a 9.3 kb segment located on the left arm of the yeast chromosome  
ribosomal protein L10.  
A;Reference number: S30013; MUID:93127732; PMID:1481574  
A;Accession: S30015  
A;Molecule type: DNA  
A;Residues: 1-1483 <PAS>  
A;Cross-references: UNIPROT:P33202; UNIPARC:UPI0000137AD6; GB:S53418; NID:G263497; PIDN:  
A;Experimental source: strain S288C  
R;Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Collea, L.; Thierry, A.; Monnier  
submitted to the Protein Sequence Database, March 1994  
A;Reference number: S37821  
A;Accession: S37821  
A;Molecule type: DNA  
A;Residues: 1-1483 <BOY>  
A;Cross-references: UNIPARC:UPI0000137AD6; EMBL:Z28010; NID:G485992; PIDN:CAA81845.1; PI  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:UFD4  
A;Cross-references: SGD:S0001493; MIPS:YKL010c  
A;Map position: 11L

Query Match 24.4%; Score 49; DB 2; Length 1483;  
Best Local Similarity 34.4%; Pred. No. 3.9e+02;  
Matches 11; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 2 SQNEVFDLSLHACIPCOLRCSSTNPPLTCQRY 33  
DB 499 SNQKFDLSLVQCLIPILVEIYTNADFDVRY 530

RESULT 61  
T27283  
hypotheical protein Y64G10A.f - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
R;Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20336  
A;Accession: T27283  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1620 <WIL>  
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:el542303; PIDN:CAB54471.1;  
A;Experimental source: clone Y64G10A  
C;Genetics:  
A;Gene: CESP:Y64G10A.f  
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 24.4%; Score 49; DB 2; Length 1620;  
Best Local Similarity 23.8%; Pred. No. 4.2e+02;  
Matches 10; Conservative 7; Mismatches 17; Indels 8; Gaps 1;

QY 1 CSQNEVFDLSLHACI-----PQLRCSSTNPPLTCQRYC 34  
DB 1409 CENGVCDSSTGSCVCPGVIQTKCEIACQSDRFGPTCEKIC 1450

RESULT 62  
T13171  
probable vitellogenin receptor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
A;Accession: T13171  
R;Schonbaum, C.P.; Lee, S.; Mahowald, A.P.  
Proc. Natl. Acad. Sci. U.S.A. 92, 1485-1489, 1995  
A;Title: The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the  
A;Reference number: Z17627; MUID:95183490; PMID:7878005

A;Accession: T13171  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1984 <SCH>  
A;Cross-references: UNIPROT:P98163; UNIPARC:UPI000013B879; EMBL:U13637; NID:G535345; PID  
C;Genetics:  
A;Gene: Y1  
A;Cross-references: FlyBase:FBgn0004649  
A;Map position: 1  
F;90-124/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;129-166/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F;184-220/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
F;227-262/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
F;266-304/Domain: LDL receptor ligand-binding repeat homology <LDL12>  
F;1025-1062/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F;1074-1109/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F;1118-1152/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;1158-1193/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F;1198-1232/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F;1243-1279/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F;1283-1318/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F;1340-1375/Domain: LDL receptor ligand-binding repeat homology <LDL9>

Query Match 24.4%; Score 49; DB 2; Length 1984;  
Best Local Similarity 33.3%; Pred. No. 5e+02;  
Matches 11; Conservative 7; Mismatches 11; Indels 4; Gaps 2;

QY 1 CSQNEVFDLSLHACIPCOLRCSSTNPPLTCOR 32  
DB 1243 CASDQYQCTSNLKLCLPFSVRCNGTT---ECPR 1272

RESULT 63  
A46019  
notch-1 protein - mouse  
N;Alternate names: notch protein  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Oct-2004  
A;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109  
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid  
Genomics 19, 259-264, 1993  
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of  
A;Reference number: A46019; MUID:93194170; PMID:8449489  
A;Accession: A46019  
A;Status: not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-2531 <DEL>  
A;Cross-references: UNIPROT:Q01705; UNIPARC:UPI000002922B; GB:Z11886; NID:G28  
A;Note: sequence extracted from NCBI backbone (NCBI:P127318)  
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; i  
submitted to the EMBL Data Library, April 1992  
A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest  
A;Reference number: S25144  
A;Accession: S25144  
A;Molecule type: mRNA  
A;Residues: 1551-2108, 'O', 2110-2114, 'ALP', 2118-2170 <FRA>  
A;Cross-references: UNIPARC:UPI0000177461; EMBL:Z11886  
R;Lardelli, M.; Lendahl, U.  
Exp. Cell Res. 204, 364-372, 1993  
A;Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety o  
A;Reference number: A49175; MUID:93178563; PMID:8440332  
A;Accession: C49175  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1161-1547 <LAR>  
A;Cross-references: UNIPARC:UPI0000177462; EMBL:X68278; NID:G287987; PIDN:CAA48339.1; i  
A;Experimental source: embryo  
A;Note: sequence extracted from NCBI backbone (NCBI:P126159)  
R;Kopan, R.; Weintraub, H.  
J. Cell Biol. 121, 631-641, 1993  
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinati  
A;Reference number: A46438; MUID:93252998; PMID:8486742  
A;Accession: B46438

A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054  
A:Cross-references: UNIPARC:UPI0000177463  
A:Experimental source: embryo  
A>Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)  
C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.  
C:Comment: This protein is one of the neurogenic proteins controlling the decision between  
C:Genetics:  
A:Gene: notch-1  
A:Map position: 2  
A:Note: proximal region of chromosome 2  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F:106-138/Domain: EGF homology <EGF1>  
F:144-175/Domain: EGF homology <EGF1>  
F:222-254/Domain: EGF homology <EGF2>  
F:261-292/Domain: EGF homology <EGF2>  
F:339-370/Domain: EGF homology <EGF3>  
F:416-449/Domain: EGF homology <EGF3>  
F:456-487/Domain: EGF homology <EGF3>  
F:494-525/Domain: EGF homology <EGF3>  
F:532-563/Domain: EGF homology <EGF3>  
F:607-638/Domain: EGF homology <EGF3>  
F:682-713/Domain: EGF homology <EGF3>  
F:757-788/Domain: EGF homology <EGF3>  
F:795-826/Domain: EGF homology <EGF3>  
F:873-904/Domain: EGF homology <EGF3>  
F:911-942/Domain: EGF homology <EGF3>  
F:949-980/Domain: EGF homology <EGF3>  
F:987-1018/Domain: EGF homology <EGF3>  
F:1025-1056/Domain: EGF homology <EGF3>  
F:1063-1094/Domain: EGF homology <EGF3>  
F:1149-1180/Domain: EGF homology <EGF3>  
F:1187-1218/Domain: EGF homology <EGF3>  
F:1233-1264/Domain: EGF homology <EGF3>  
F:1352-1383/Domain: EGF homology <EGF3>  
F:1391-1425/Domain: EGF homology <EGF3>  
F:1917-1948/Domain: ankyrin repeat homology <AN1>  
F:1949-1981/Domain: ankyrin repeat homology <AN2>  
F:1983-2015/Domain: ankyrin repeat homology <AN3>  
F:2016-2048/Domain: ankyrin repeat homology <AN4>  
F:2049-2081/Domain: ankyrin repeat homology <AN5>  
  
Query Match 24.4%; Score 49; DB 2; Length 2531;  
Best Local Similarity 40.7%; Pred. No. 6.2e+02;  
Matches 11; Conservative 4; Mismatches 10; Indels 2; Gaps 1;  
  
QY 10 LLHACI--PQLRCSSNTPPLTCQRYC 34  
DB 372 LKHACISNFCNCGSNCNTNPNVNGKRIC 398  
  
RESULT 64  
T10053  
laminin alpha 5 chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T10053  
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.  
Submitted to the EMBL Data Library, November 1997  
A:Reference number: Z16923  
A:Accession: T10053  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-3635 <MIN>  
A:Cross-references: UNIPROT:Q61001; UNIPARC:UPI000004C5E9; EMBL:U37501; NID:g2599231; PIDN:CAA16417.1  
C:Genetics:  
A:Gene: Lama5  
C:Keywords: Basement membrane; cell binding; extracellular matrix  
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>  
F:1942-1970/Domain: EGF homology <EGF>  
  
Query Match 24.4%; Score 49; DB 2; Length 3635;

Best Local Similarity 26.0%; Pred. No. 8.4e+02;  
Matches 13; Conservative 5; Mismatches 14; Indels 18; Gaps 2;  
  
QY 1 CSONEYFDS---LLHACIPQC-----LRCSNTPPLTCQR 32  
DB 1763 CAPGYVRTKGLFLGRCVPCQCHGHSRCLPGSGICVCGQHNTGQCQR 1812  
  
RESULT 65  
T27297  
hypothetical protein Y68A4A.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27297  
R:Steward, C.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z20340  
A:Accession: T27297  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-474 <WIL>  
A:Cross-references: UNIPROT:Q9XXQ2; UNIPARC:UPI00000783D7; EMBL:AL021503; PIDN:CAA16417.1  
A:Experimental source: clone Y68A4A  
C:Genetics:  
A:Gene: CESP:Y68A4A.5  
A:Map position: 5  
A:Introns: 47/2; 80/3; 145/3; 181/2; 196/3; 238/2; 269/2; 306/3; 342/2; 357/3; 418/3  
  
Query Match 24.1%; Score 48.5; DB 2; Length 474;  
Best Local Similarity 42.9%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 8; Indels 1; Gaps 1;  
  
QY 14 CIPCQLRCSSNTPPLTCQRYC 34  
DB 357 CLPCQ-TCTFTDPMGAHASC 376  
  
RESULT 66  
AB0N51  
serum albumin 1 precursor - Atlantic salmon  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: A36238; S13079  
R:Byrnes, L.; Gannon, F.  
DNA Cell Biol. 9, 647-655, 1990  
A:Title: Atlantic salmon (Salmo salar) serum albumin: cDNA sequence, evolution, and tissue  
A:Reference number: A36238; MUID:91083837; PMID:2261082  
A:Accession: A36238  
A:Molecule type: mRNA  
A:Residues: 1-608 <BYR>  
A:Cross-references: UNIPROT:P21848; UNIPARC:UPI00001257B6; GB:X52397; NID:g64375; PIDN:CI  
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, iron  
mones (weak bonds with these hormones promote their transfer across the membranes), thyroxine  
C:Superfamily: serum albumin; serum albumin repeat homology  
C:Keywords: carrier protein; duplication; plasma  
F:1-14/Domain: signal sequence #status predicted <SIG>  
F:15-18/Domain: propeptide #status predicted <PRO>  
F:19-608/Product: serum albumin #status predicted <MAT>  
F:23-196/Domain: serum albumin repeat homology <SA1>  
F:215-390/Domain: serum albumin repeat homology <SA2>  
F:411-591/Domain: serum albumin repeat homology <SA3>  
F:26-72, 71-80, 93-108, 107-118, 142-187, 186-195, 218-264, 263-271, 283-299, 298-309, 336-381, 380-  
  
Query Match 24.1%; Score 48.5; DB 1; Length 608;  
Best Local Similarity 34.4%; Pred. No. 2.1e+02;  
Matches 11; Conservative 5; Mismatches 9; Indels 7; Gaps 1;  
  
QY 8 DSLHACIP-----COLRCSSNTPPLTCQR 32  
DB 51 DSTLGDVLPLIAEALAMGVKCCSDTPPEDCER 82  
  
RESULT 67



```
AB0NS2
serum albumin 2 precursor - Atlantic salmon
C;Species: Salmo salar (Atlantic salmon)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A46757; S30594
R;Byrnes, L.
submitted to the EMBL Data Library, June 1991
A;Reference number: A46757
A;Accession: A46757
A;Molecule type: mRNA
A;Residues: 1-608 <BYR>
A;Cross-references: UNIPROT:Q03156; UNIPARC:UPI00001257BB; EMBL:X60776; NID:G64349; PIDN
R;Byrnes, L.; Gannon, F.
Gene 120, 319-320, 1992
A;Title: Sequence analysis of a second cDNA encoding Atlantic salmon (Salmo salar) serum
A;Reference number: S30594; MUID:93013056; PMID:11398147
A;Contents: annotation
A;Note: only a list of differences from sequence A36238 is shown
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
mones (weak bonds with these hormones promote their transfer across the membranes), thyro
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; plasma
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-18/Domain: propeptide #status predicted <PRO>
F;19-608/Product: serum albumin #status predicted <MAT>
F;23-196/Domain: serum albumin repeat homology <SA1>
F;215-390/Domain: serum albumin repeat homology <SA2>
F;411-591/Domain: serum albumin repeat homology <SA3>
F;26-72,71-80,93-108,107-118,142-187,186-195,218-264,263-271,283-299,309,336-381,380
Query Match 24.1%; Score 48.5; DB 1; Length 608;
Best Local Similarity 34.4%; Pred. No. 2.1e+02;
Matches 11; Conservative 5; Mismatches 9; Indels 7; Gaps 1;

Oy 8 DSLHACIP-----COLRCSSNTPTLTCOR 32
||| ||| :||| ||| |||
Db 51 DSTGLDVLPLAEALMGVKCSPTPEDCR 82
||| ||| :||| ||| |||

RESULT 68
hypotheical protein F56A6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 23-Mar-2001
C;Accession: T33079
R;Murray, J.; Rohlfing, T.; O'Neal, D.; Wilson, R.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid F56A6.
A;Reference number: Z21279
A;Accession: T33079
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1846 <MUR>
A;Cross-references: UNIPARC:UPI000017763D; EMBL:AF067217; PIDN:AAC17015.1; GSPDB:GN00019
A;Experimental source: strain Bristol N2; clone F56A6
C;Genetics:
A;Gene: CESP:F56A6.2
A;Map position: 1
A;Introns: 71/1; 165/3; 247/2; 335/2; 356/2; 389/3; 441/3; 497/3; 539/1; 607/3; 636/3; 6
06/1; 1714/3; 1756/2
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zeta

Query Match 24.1%; Score 48.5; DB 2; Length 1846;
Best Local Similarity 26.5%; Pred. No. 5.4e+02;
Matches 9; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

Oy 1 CSQNEYFDSLHACIPCOLRCSSNTPTPLT---CQ 31
||| :||| :||| |||
Db 1457 CNQLIWHHEKLYTCVACRISCHKCKQPKVTHPCQ 1490
||| :||| :||| |||

RESULT 69
T14119
seven-pass transmembrane receptor protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14119
R;Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
submitted to the EMBL Data Library, October 1997
A;Description: The Celser family of novel evolutionarily conserved seven-pass transmembran
A;Reference number: Z17881
A;Accession: T14119
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3034 <HAD>
A;Cross-references: UNIPROT:O35161; UNIPARC:UPI000002931C; EMBL:AF031572; NID:G3800735; I
C;Genetics:
A;Gene: Celser1
A;Map position: 15
C;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>

Query Match 24.1%; Score 48.5; DB 2; Length 3034;
Best Local Similarity 25.5%; Pred. No. 8.3e+02;
Matches 12; Conservative 4; Mismatches 18; Indels 13; Gaps 2;

Oy 1 CSQNEYFDSLHACIPCOLRCSSNTPTPLTCQ-----RYC 34
||| ||| :||| ||| |||
Db 2002 CKENYKPPAQDACLPCDCFFGHGSHSRACMDTGCQACKPGVIGRQC 2048
||| ||| :||| ||| |||

RESULT 70
JN0380
trypsin inhibitor IV - sea anemone (Radianthus macrodactylus)
C;Species: Radianthus macrodactylus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
C;Accession: JN0380
R;Zykova, T.A.; Vinokurov, L.M.; Markova, L.F.; Kozlovskaya, E.P.; Elyakov, G.B.
Bioorg. Khim. 11, 293-301, 1985
A;Title: Amino-acid sequence of trypsin inhibitor IV from Radianthus macrodactylus.
A;Reference number: JN0380
A;Accession: JN0380
A;Molecule type: protein
A;Residues: 1-56 <ZYK>
A;Cross-references: UNIPROT:P16344; UNIPARC:UPI000012DA5F
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;4-54/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;4-54,13-37,29-50/Disulfide bonds: #status predicted

Query Match 23.9%; Score 48; DB 2; Length 56;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 CSQNEYFDSLHAC 14
||| ||| |||
Db 37 CEGSNYVDEKLHAC 50
||| ||| |||

RESULT 71
C89046
protein C10G8.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89046
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: C89046
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <STO>
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Search completed: December 21, 2005, 16:11:38  
Job time : 22.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:56:49 ; Search time 117.2 Seconds

(without alignments)  
204.675 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41

Perfect score: 201

Sequence: 1 CSQNEYPDLSLHACIPQLRCSSTPTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	184	1	TNR17_HUMAN
2	201	100.0	184	2	QPEA6_HUMAN
3	136	67.7	185	1	TNR17_MOUSE
4	72.5	36.1	499	2	Q88714_MOUSE
5	72.5	36.1	1674	2	Q80218_MOUSE
6	72.5	36.1	2850	2	Q80T03_MOUSE
7	71.5	35.6	74	2	Q8U84_MOUSE
8	71.5	35.6	140	2	Q8U83_MOUSE
9	71.5	35.6	249	1	TR13B_MOUSE
10	71.5	35.6	249	2	Q8U82_MOUSE
11	68.5	34.1	1569	2	Q6W4X9_HUMAN
12	67.5	33.6	1877	1	PCSK5_MOUSE
13	66.5	33.1	293	1	TR13B_HUMAN
14	66.5	33.1	293	2	Q8F3F6_HUMAN
15	65.5	32.6	1025	2	Q7R6J7_GIALA
16	64.5	32.1	5374	2	Q99ND0_MOUSE
17	64.5	32.1	5376	1	ZAN_MOUSE
18	64	31.8	762	2	Q4I0Y5_GIBBE
19	63.5	31.6	799	2	Q50LY7_ENTHI
20	63.5	31.6	802	2	Q50Y51_ENTHI
21	63	31.3	1150	2	Q50PT4_ENTHI
22	62.5	31.1	1294	2	Q7QGV0_ANOGA
23	61.5	30.6	3005	2	Q8BFG4_PART
24	61	30.3	966	2	Q23378_CAEEL
25	61	30.3	1560	2	Q5USG7_HUMAN
26	60	29.9	830	2	Q4TY8_tetradon n
27	60	29.9	867	1	SSPO_BOVIN
28	60	29.9	5146	2	Q8SPM4_BOVIN
29	59.5	29.6	353	2	Q8SZ58_DROME
30	59.5	29.6	353	2	Q9VW81_DROME
31	59.5	29.6	484	2	Q5CZ68_HUMAN

Q8NAV8	homo sapien
Q5CZB3	homo sapien
Q55NL5	cryptococcu
Q8NAU9	homo sapien
Q81Z06	homo sapien
Q7Z5T8	homo sapien
Q86UZ9	homo sapien
Q81X30	homo sapien
Q5HYA8	homo sapien
Q84Q3	tetraodon n
Q9GYR5	caenorhabdi
Q51E46	entamoeba h
Q5DD86	schistosoma
Q68F99	mus musculu
Q66PY1	mus musculu
Q8BR19	mus musculu
Q9D840	mus musculu
Q8R4W8	mus musculu
Q678B7	lymphocyeta
Q26489	spodoptera
F07851	ascaris suu
Q5BI10	drosophila
P30432	drosophila
Q51AP4	entamoeba h
Q9MAM0	arabidopsis
Q61V24	caenorhabdi
Q7R165	giardia lam
Q26566	schistosoma
Q8WRP4	moneteiga br
Q51EF3	entamoeba h
Q60WC9	caenorhabdi
Q8CFA7	mus musculu
Q9D351	mus musculu
Q6P233	mouse
Q9PVD4	xenopus lae
Q4K1X7	xenopus lae
Q6NUF1	xenopus lae
Q60K18	caenorhabdi
Q28903	sus scrofa
Q9EP28	hepatitis c
Q9E40	drosophila
Q41FW6	gibberella
Q86WK8	homo sapien
Q96DN2	homo sapien
Q92U00	arabidopsis
Q6IRM7	xenopus lae
Q9VL76	drosophila
Q87M85	vibrio para
Q18118	caenorhabdi
Q924K7	meriones un
Q81YJ8	homo sapien
Q6P0M3	homo sapien
Q86JV7	debaromyce
Q9ULT0	homo sapien
Q17970	caenorhabdi
Q6Q157	rattus norv
Q964D1	entamoeba h
Q50RX4	entamoeba h
Q964D2	entamoeba h
Q517S0	entamoeba h
Q50ZK2	entamoeba h
Q993K9	callitrichi
Q50RX0	entamoeba h
Q820M9	caenorhabdi
Q50Y64	entamoeba h
Q4QCP3	leishmania
Q9EP23	hepatitis c
Q4WC19	aspergillus
Q50M54	entamoeba h
Q9C091	homo sapien
Q5ICE3	entamoeba h
Q50SS7	entamoeba h
O57484	gallus gall



251	51	25.4	448	2	Q5EF27	CHICK
252	51	25.4	484	2	Q7UM25	RHORA
253	51	25.4	489	2	Q4WL45	ASPFU
254	51	25.4	622	2	Q7QWD2	GIALA
255	51	25.4	641	2	Q9FV53	ARATH
256	51	25.4	645	2	Q8VY20	ARATH
257	51	25.4	653	2	Q9S9J8	ARATH
258	51	25.4	675	2	Q94LU3	ORYSA
259	51	25.4	746	2	Q9SJ15	ARATH
260	51	25.4	911	2	Q68KE9	XENLA
261	51	25.4	911	2	Q5G5T9	XENLA
262	51	25.4	949	2	Q4S2B5	TETNG
263	51	25.4	1010	2	Q59166	BRARE
264	51	25.4	1010	2	Q5G872	BRARE
265	51	25.4	1017	2	Q84P66	ORYSA
266	51	25.4	1117	2	Q652W3	ORYSA
267	51	25.4	2774	2	Q4Z799	PLASMODIUM
268	51	25.4	2980	2	Q8IAK3	PLAF7
269	51	25.4	3087	2	Q8WRD2	PLABE
270	51	25.4	3622	2	Q6RG85	PARTE
271	51	25.4	4680	2	Q7PV66	ANOGEA
272	50.5	25.1	37	2	Q9SDS1	PHYAM
273	50.5	25.1	102	2	Q6PIK8	HUMAN
274	50.5	25.1	146	2	Q9EP20	9HEPC
275	50.5	25.1	146	2	Q9EP32	9HEPC
276	50.5	25.1	158	2	Q5XQV7	9HEPC
277	50.5	25.1	188	2	Q6IM32	CABBR
278	50.5	25.1	263	2	Q9WDU5	9HIV1
279	50.5	25.1	263	2	Q9WDU8	9HIV1
280	50.5	25.1	263	2	Q9WDV0	9HIV1
281	50.5	25.1	263	2	Q9WDV6	9HIV1
282	50.5	25.1	263	2	Q9WDV8	9HIV1
283	50.5	25.1	263	2	Q9WDW7	9HIV1
284	50.5	25.1	263	2	Q9WDW8	9HIV1
285	50.5	25.1	263	2	Q9WDW9	9HIV1
286	50.5	25.1	263	2	Q9WDX0	9HIV1
287	50.5	25.1	263	2	Q9WDX6	9HIV1
288	50.5	25.1	263	2	Q9WE18	9HIV1
289	50.5	25.1	263	2	Q9WE19	9HIV1
290	50.5	25.1	263	2	Q9WEJ0	9HIV1
291	50.5	25.1	263	2	Q9WEJ1	9HIV1
292	50.5	25.1	263	2	Q9WEJ2	9HIV1
293	50.5	25.1	263	2	Q9WEJ4	9HIV1
294	50.5	25.1	263	2	Q9WEJ5	9HIV1
295	50.5	25.1	263	2	Q9WEJ7	9HIV1
296	50.5	25.1	263	2	Q9WEJ9	9HIV1
297	50.5	25.1	263	2	Q9WEJ3	9HIV1
298	50.5	25.1	325	2	Q5ZLJ8	CHICK
299	50.5	25.1	599	2	Q4TG04	BRARE
300	50.5	25.1	610	1	C4BP_BOVIN	

ALIGNMENTS

RESULT 1  
 TNR17 HUMAN  
 ID TNR17 HUMAN STANDARD; PRT; 184 AA.  
 AC Q02223;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).  
 DE Name=TNFRSF17; Synonym=BCM, BCMA;  
 GN Homo sapiens (Human)  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND CHROMOSOMAL TRANSLOCATION.  
 RC TISSUE=Lymph node, and Peripheral blood leukocyte;

RX MEDLINE=93010984; PubMed=1396583;  
 RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,  
 RA Larsen C.-J., Tsapis A.,  
 RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene  
 by a t(4;16)(q26;q33) translocation in a malignant T cell lymphoma.";  
 RL EMBO J. 11:3897-3904(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94218235; PubMed=8165126;  
 RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;  
 RT "The BCMA gene, preferentially expressed during B lymphoid maturation,  
 is bidirectionally transcribed.";  
 RL Nucleic Acids Res. 22:1147-1154(1994).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;  
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,  
 RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,  
 RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,  
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
 RT "Genome duplications and other features in 12 Mb of DNA sequence from  
 human chromosome 16p and 16q.";  
 RL Genomics 60:295-308(1999).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANT THR-153.  
 RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/s1/gene/6363770;  
 RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;  
 RT "Presence of four major haplotypes in human BCMA gene: lack of  
 association with systemic lupus erythematosus and rheumatoid  
 arthritis.";  
 RL Genes Immun. 2:276-279(2001).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65;  
 VAL-75; ASN-81 AND SER-165.  
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,  
 RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;  
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
 of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.  
 RX MEDLINE=20363816; PubMed=10903733;  
 RA Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C.,  
 RA Inoue J.-I., Devergne O., Tsapis A.;  
 RT "TNF receptor family member BCMA (B cell maturation) associates with  
 TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and  
 activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-  
 activated protein kinase.";  
 RL J. Immunol. 165:1322-1330(2000).  
 RN [7]  
 RP FUNCTION.  
 RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;  
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,  
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,  
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,  
 RA Harrison K., Kindvogel W., Clegg C.H.;  
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell  
 autoimmune disease.";  
 RL Nature 404:995-999(2000).  
 RN [8]  
 RP FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.  
 RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;  
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,  
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;  
 RT "APRIL and TRAIL-I and receptors BCMA and TACI: system for regulating  
 humoral immunity.";  
 RL Nat. Immunol. 1:252-256(2000).  
 RN [9]  
 RP INTERACTIONS WITH TRAF5 AND TRAF6.  
 RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;  
 RA Shu H.-B., Johnson H.;

RT "B cell maturation protein is a receptor for the tumor necrosis factor  
family member TNF- $\alpha$ .";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).  
CC -1- FUNCTION: Receptor for TNF $\alpha$ /BLYS/BAFF and TNFSF13/APRIL.  
CC Promotes B-cell survival and plays a role in the regulation of  
CC humoral immunity. Activates NF-kappa-B and JNK.  
CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
CC  
CC -1- INTERACTION:  
CC Q9Y275:TNFSF13B; NdeExp=1; IntAct=EBI-519945, EBI-519169;  
CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane  
CC and perinuclear Golgi-like structures.  
CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-  
CC cells or monocytes.  
CC  
CC -1- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a  
CC form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation  
CC t(4;16)(q26;p13) with IL2.  
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC ENBL; Z14954; CAA78679.1; -; mRNA.  
CC ENBL; Z29575; CAA82690.1; -; mRNA.  
CC ENBL; Z29574; CAA82690.1; -; Genomic DNA.  
CC ENBL; U95742; AAB67251.1; -; Genomic DNA.  
CC ENBL; AB052772; BAB60895.1; -; Genomic DNA.  
CC ENBL; AY509112; AAR84240.1; -; Genomic DNA.  
CC PIR; S43486; S43486.  
CC PDB; 1Q0D; X-ray; K/L/M/N/O/P/Q/R=8-46.  
CC PDB; 1XU2; X-ray; R/S/T=5-51.  
CC IntAct; Q02223; -.  
CC DR HGNC; HGNC:11913; TNFRSF17.  
CC DR MIM; 109545; -.  
CC DR GO; GO:0016021; C: integral to membrane; TAS.  
CC DR GO; GO:0005886; C: plasma membrane; TAS.  
CC DR GO; GO:0004872; F: receptor activity; TAS.  
CC DR GO; GO:0008283; P: cell proliferation; TAS.  
CC DR GO; GO:0007275; P: development; TAS.  
CC DR GO; GO:0007165; P: signal transduction; TAS.  
CC DR InterPro; IPR001368; TNFR\_C6.  
CC DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
CC DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE NEG.  
CC 3D-structure: Chromosomal translocation; Immune response;  
CC Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.  
FT TOPO\_DOM 1 54 Extracellular (Potential).  
FT TRANSMEM 55 77 Signal-anchor for type III membrane  
FT TOPO\_DOM 78 184 protein (Potential).  
FT REPEAT 7 41 Cytoplasmic (Potential).  
FT SITE 3 4 Breakpoint for translocation to form  
FT IL2/TNFRSF17 oncogene.  
FT DISULFID 8 21 By similarity.  
FT DISULFID 24 37 By similarity.  
FT DISULFID 28 41 By similarity.  
FT VARIANT 54 54 A -> V.  
FT VARIANT 65 65 I -> V.  
FT VARIANT 75 75 F -> V.  
FT VARIANT 81 81 S -> N (in dbSNP:373496).  
FT VARIANT 153 153 A -> T.  
FT VARIANT 165 165 C -> S.  
FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;  
Query Match 100.0%; Score 201; DB 1; Length 184;

Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLLHACIPQCLRCSSNTPTLTQRYC 34  
DB 8 CSQNEYFDSLLHACIPQCLRCSSNTPTLTQRYC 41  
RESULT 2  
Q6PE46 HUMAN  
ID Q6PE46 HUMAN PRELIMINARY; PRT; 184 AA.  
AC Q6PE46;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Tumor necrosis factor receptor superfamily, member 17.  
GN Name=TNFRSF17;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pooled;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pooled;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC058291; AAH58291.1; -; mRNA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
KW Receptor.  
SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;  
Query Match 100.0%; Score 201; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLLHACIPQCLRCSSNTPTLTQRYC 34  
DB 8 CSQNEYFDSLLHACIPQCLRCSSNTPTLTQRYC 41  
RESULT 3  
TNFR17\_MOUSE  
ID TNFR17\_MOUSE STANDARD; PRT; 185 AA.  
AC O88472;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 17 (B-cell



DE maturation protein).

GN Name=TNfrsf17; Synonym=Bcm, Bcm;

OS Mus musculus (Mouse);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP STRAIN=BALEB/C; TISSUE=Spleen;

RC STRAIN=BALEB/C; TISSUE=Spleen;

RX MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693;

RA Madry C., Laubi Y., Callebaut I., Roussel J., Hatzoglu A.,

RA Le Coniat M., Morion J.P., Berger R., Taapis A.;

RT "The characterization of murine BCMA gene defines it as a new member

RT of the tumor necrosis factor receptor superfamily.";

RL Inc. Immunol. 10:1693-1702(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,

RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perte G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [3]

RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1).

RC STRAIN=C57BL/6J; TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Receptor for TNFSF13B/BlyS/BAFF and TNFSF13/APRIL.

CC Promotes B-cell survival and plays a role in the regulation of

CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).

CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by

CC similarity).

CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=O88472-1; Sequence=Displayed;

CC Name=2;

CC IsoId=O88472-2; Sequence=VSP\_006507;

CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and

CC heart, and at lower levels in kidney and lung.

CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL: AF061505; AAC23799.1; -; mRNA.

CC EMBL: AK020247; BAB32038.1; -; mRNA.

CC EMBL: BC027519; AAH27519.1; -; mRNA.

CC HSSP: Q02223; 1QDD.

CC Ensembl: ENSMUSG00000022496; Mus musculus.

CC MGI: MGI-1343050; Tnfref17.

CC GO: GO:0016021; C:integral to membrane; TAS.

CC InterPro: IPR001368; TNFR\_C6.

CC PROSITE: PS00652; TNFR\_NGFR\_1; FALSE NEG.

CC PROSITE: PS00500; TNFR\_NGFR\_2; FALSE NEG.

CC Alternative splicing; Immune response; Receptor; Signal-anchor;

CC Transmembrane. 1 49 Extracellular (Potential).

CC TOFO\_DOM 50 70 Signal-anchor for type III membrane

CC TRANSMEM 50 70 protein (Potential).

CC FT REPEAT 71 185 Cytoplasmic (Potential).

CC FT DISULFID 4 36 TNFR-Cys.

CC FT DISULFID 5 18 By similarity.

CC FT DISULFID 21 32 By similarity.

CC FT DISULFID 25 36 By similarity.

CC FT VARSPLIC 87 91 Missing (in isoform 2).

CC FT SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A9E CRC64;

Query Match 67.7%; Score 136; DB 1; Length 185;

Best Local Similarity 70.6%; Pred. No. 7.4e-10;

Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Oy 1 CSONEYFDSLHLHACIPCOLRCSSNTPLTTCORYC 34

Db 5 CFHSEYFDSLHLHACKPHLRCSN--PPATCQPYC 36

-----

RESULT 4

O88714 MOUSE

ID O88714 MOUSE PRELIMINARY; PRT; 499 AA.

AC O88714;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Gastric mucin-like protein (Fragment).

DE Name=Muc6; Synonym=gastrectic mucin-like;

GN Name=Musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Stomach;

RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,



Qy 1 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQRYC 34  
 Db 6 CPKQYWDSSRKSCVSCALTCQRS-ORTCTDFC 38

RESULT 8  
 Q5U83 MOUSE  
 ID Q5U83\_MOUSE PRELIMINARY; PRT; 140 AA.  
 AC Q5U83;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily, member 13b  
 DE (Fragment).  
 DE Name=TNFRsf13b; ORFNames=RP23-5512.2-003;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_taxid=10090;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Holt K.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL646093; CA125895.1; -; Genomic DNA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON TER 140 140  
 SQ SEQUENCE 140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;

Query Match 35.6%; Score 71.5; DB 2; Length 140;  
 Best Local Similarity 35.3%; Pred. No. 0.17;  
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQRYC 34  
 Db 6 CPKQYWDSSRKSCVSCALTCQRS-ORTCTDFC 38

RESULT 9  
 TR13B MOUSE  
 ID TR13B\_MOUSE STANDARD; PRT; 249 AA.  
 AC Q9ET35; Q9DB23;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane  
 DE activator and CAML interacto).  
 GN Name=TNFRsf13b; Synonyms=taci;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_taxid=10090;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76989;  
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;  
 RT "Identification of a receptor for BlyS demonstrates a crucial role in  
 RT humoral immunity.";  
 RL Nat. Immunol. 1:37-41 (2000).  
 [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=22354683; PubMed=12466951; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,  
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 [3]  
 RP FUNCTION.  
 RX MEDLINE=20341628; PubMed=1080535; DOI=10.1084/jem.192.1.137;  
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,  
 Theill L.E., Colombero A., Solovye I., Lee F., McCabe S., Elliott R.,  
 Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,  
 Meng S.-Y., Boyle W.J., Hsu H.;  
 RT "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis  
 RT factor family member involved in B cell regulation.";  
 RL J. Exp. Med. 192:137-143 (2000).  
 [4]  
 RP FUNCTION.  
 RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;  
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,  
 Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;  
 RT "TAC1-ligand interactions are required for T cell activation and  
 RT collagen-induced arthritis in mice.";  
 RL Nat. Immunol. 2:632-637 (2001).  
 CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS  
 CC that binds both ligands with similar high affinity. Mediates  
 CC calcineurin-dependent activation of NF-AT, as well as activation  
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-  
 CC cell function and the regulation of humoral immunity (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal  
 CC domain of CAMLG with its C-terminus (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).  
 CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.  
 -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
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 CC EMBL; AF257673; AAG00081.1; -; mRNA.  
 CC EMBL; AK004668; BAB23457.1; -; mRNA.  
 CC Ensembl; ENSMUSG0000010142; Mus musculus.  
 CC MGI; MGI:1889411; Tnfrsf13b.  
 CC GO; GO:0009897; C:external side of plasma membrane; IDA.  
 CC GO; GO:0005887; C:integral to plasma membrane; IDA.  
 CC GO; GO:0001782; P:B cell homeostasis; IMP.  
 CC GO; GO:0030889; P:negative regulation of B cell proliferation; IMP.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
 CC PROSITE; PS00505; TNFR\_NGFR\_2; FALSE NEG.  
 KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.  
 FT TOPO\_DOM 1 128  
 FT Signal-anchor for type III membrane  
 FT TRANSMEM 129 149  
 FT protein (Potential).







RA Maruyama K., Sugano S.;  
 RT "Oligo-capping : a simple method to replace the cap structure of  
 RT eucaryotic mRNAs with oligoribonucleotides.";  
 RL Gene 138:171-174 (1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Small intestine;  
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;  
 RT "Construction and characterization of a full length-enriched and a 5'-  
 RT end-enriched cDNA library.";  
 RL Gene 200:149-156 (1997).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE  
 RC TISSUE=Small intestine;  
 RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;  
 RT Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AK223453; BAD97173.1; -; mRNA.  
 KW Receptor.  
 FT NON TER  
 SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;  
 Query Match 33.1%; Score 66.5; DB 2; Length 293;  
 Best Local Similarity 32.4%; Pred. No. 1.6;  
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;  
 Qy 1 CSONEYFDSLHACIPCOLRCSSTPPLTCQRYC 34  
 Db 34 CPBQYWDPLLGTCMSCKTICNHQS-QRTCAAF 66  
 RESULT 15  
 ID Q7R6J7 GIALA PRELIMINARY; PRT; 1025 AA.  
 AC Q7R6J7;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE GLP 170 141434 144511.  
 OS Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.  
 OX NCBI\_TaxID=184922;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AACB0100001; EAA43000.1; -; Genomic\_DNA.  
 DR HSP; O9S7B3; 1EHD.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; UNKNOWN\_1.  
 SQ SEQUENCE 1025 AA; 109044 MW; 36281DF3FE2DD843 CRC64;  
 Query Match 32.6%; Score 65.5; DB 2; Length 1025;  
 Best Local Similarity 36.1%; Pred. No. 7.9;  
 Matches 13; Conservative 5; Mismatches 13; Indels 5; Gaps 1;  
 Qy 1 CSONEYFDSLHACIPCOLRCSSTP-----LTCQ 31  
 Db 79 CTDDFYLDLRFCCFSCHSCSTCGPSHFDCLTGR 114  
 RESULT 16  
 Q99ND0 MOUSE  
 ID Q99ND0 MOUSE PRELIMINARY; PRT; 5374 AA.  
 AC Q99ND0;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE ZAN (Zonadhesin).  
 GN Name=Zan;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/Sv;  
 RX MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;  
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,  
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,  
 RA Miller W., Koop B.F.;  
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human  
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";  
 RL Nucleic Acids Res. 29:1352-1365 (2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/Sv;  
 RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF312033; AAK28824.1; -; Genomic\_DNA.  
 DR EMBL; AY046056; AAL04416.1; -; Genomic\_DNA.  
 DR HSP; Q90248; 1HX2.  
 DR MGI; MGI:106656; ZAN.  
 DR GO; GO:0016020; C.membrane; IEA.  
 DR GO; GO:0007339; P.binding of sperm to zona pellucida; IEA.  
 DR GO; GO:0007155; P.cell adhesion; IEA.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR003645; Fol\_N.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR000998; MAM.  
 DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
 DR InterPro; IPR003328; TILA\_Cysrich.  
 DR InterPro; IPR001007; VWF\_C.  
 DR InterPro; IPR001846; VWF\_D.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00629; MAM; 3.  
 DR Pfam; PF01826; TIL; 25.  
 DR Pfam; PF02345; TIL\_assoc; 25.  
 DR Pfam; PF00094; VWD; 4.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00274; FOLN; 20.  
 DR SMART; SM00137; MAM; 3.  
 DR SMART; SM00214; VWC; 4.  
 DR SMART; SM00216; VWD; 4.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 18.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS00060; MAM\_2; 3.  
 DR PROSITE; PS00060; MAM\_2; 3.  
 SQ SEQUENCE 5374 AA; 579545 MW; 90D2D8CFE5DE24EB CRC64;  
 Query Match 32.1%; Score 64.5; DB 2; Length 5374;  
 Best Local Similarity 35.1%; Pred. No. 58;  
 Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;  
 Qy 1 CSONEYFDSLHACIPCOLRCSSTP--PLTCQRYC 34  
 Db 3298 CPTNSQFTDCLPSCVPCSNRCEVTPSPVSSCREG 3334  
 RESULT 17  
 ZAN MOUSE  
 ID ZAN MOUSE STANDARD; PRT; 5376 AA.  
 AC O89799; O08647;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Zonadhesin precursor.  
 GN Name=Zan;

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
RN NCBI\_TaxID=10090;  
RN [1]\_NUCLEOTIDE SEQUENCE.  
RP TISSUE=Testis;  
RC MEDLINE=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415;  
RX Gao Z., Garbers D.L.;  
RA "Species diversity in the structure of zonadhesin, a sperm-specific  
RT membrane protein containing multiple cell adhesion molecule-like  
RT domains";  
RL J. Biol. Chem. 273:3415-3421(1998).  
RN [2]  
RN NUCLEOTIDE SEQUENCE OF 4864-5376.  
RP TISSUE=Testis;  
RC MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620;  
RX Gao Z., Harumi T., Garbers D.L.;  
RA "Chromosome localization of the mouse zonadhesin gene and the human  
RT zonadhesin gene (ZAN).";  
RL Genomics 41:119-122(1997).  
CC -1- FUNCTION: Binds in a species-specific manner to the zona pellucida  
CC of the egg. May be involved in gamete recognition and/or  
CC signaling.  
CC -1- SUBUNIT: Probably forms covalent oligomers.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the  
CC apical region of the sperm head.  
CC -1- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.  
CC -1- DOMAIN: The MAM domains probably mediate sperm adhesion to the  
CC zona pellucida.  
CC -1- DOMAIN: During sperm migration through the reproductive tracts,  
CC the mucin-like domain might inhibit inappropriate trapping of  
CC spermatozoa or promoting adhesion to the oviductal isthmus.  
CC -1- DOMAIN: The VWFD domain 2 may mediate covalent oligomerization (By  
CC similarity).  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
CC -1- SIMILARITY: Contains 3 MAM domains.  
CC -1- SIMILARITY: Contains 25 VWFD domains.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; U97068; AAC26680.1; -; mRNA.  
DR EMBL; U83190; AAC53125.1; -; mRNA.  
DR PIR; T42215; T42215.  
DR HSSP; Q90248; IHX2.  
DR MGI; MGI:106656; Zan.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR004153; CKXC repeat.  
DR InterPro; IPR003341; DUF135\_Cys\_rich.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TiL.  
DR InterPro; IPR003328; TiLa\_Cysrich.  
DR InterPro; IPR001846; VWFD.  
DR Pfam; PF02363; C\_tripleX; 18.  
DR Pfam; PF03128; CKXC; 11.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00629; MAM; 3.  
DR Pfam; PF01826; TiL; 25.  
DR Pfam; PF02345; TiL\_assoc; 25.  
DR Pfam; PF00094; VWD; 4.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 18.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS00600; MAM\_2; 3.

KW Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 5376 Zonadhesin.  
FT TOPO\_DOM 18 5310 Extracellular (Potential).  
FT TRANSMEM 5311 5337 Potential.  
FT TOPO\_DOM 5338 5376 Cytoplasmic (Potential).  
FT DOMAIN 210 210 MAM 1.  
FT DOMAIN 215 374 MAM 2.  
FT DOMAIN 377 542 MAM 3.  
FT DOMAIN 1171 1280 VWFD 1 (partial).  
FT DOMAIN 1281 1669 VWFD 2.  
FT DOMAIN 1670 2056 VWFD 3.  
FT DOMAIN 2057 2459 VWFD 4.  
FT DOMAIN 2460 2579 VWFD 5 (partial).  
FT DOMAIN 2580 2699 VWFD 6 (partial).  
FT DOMAIN 2700 2819 VWFD 7 (partial).  
FT DOMAIN 2820 2939 VWFD 8 (partial).  
FT DOMAIN 2940 3059 VWFD 9 (partial).  
FT DOMAIN 3060 3179 VWFD 10 (partial).  
FT DOMAIN 3180 3299 VWFD 11 (partial).  
FT DOMAIN 3300 3416 VWFD 12 (partial).  
FT DOMAIN 3417 3536 VWFD 13 (partial).  
FT DOMAIN 3537 3656 VWFD 14 (partial).  
FT DOMAIN 3657 3776 VWFD 15 (partial).  
FT DOMAIN 3777 3892 VWFD 16 (partial).  
FT DOMAIN 3893 4028 VWFD 17 (partial).  
FT DOMAIN 4029 4148 VWFD 18 (partial).  
FT DOMAIN 4149 4263 VWFD 19 (partial).  
FT DOMAIN 4264 4283 VWFD 20 (partial).  
FT DOMAIN 4384 4503 VWFD 21 (partial).  
FT DOMAIN 4504 4623 VWFD 22 (partial).  
FT DOMAIN 4624 4743 VWFD 23 (partial).  
FT DOMAIN 4744 4863 VWFD 24 (partial).  
FT DOMAIN 4864 5261 VWFD 25.  
FT DOMAIN 5259 5295 EGF-like.  
FT REGION 547 1170 80 X heptapeptide repeats (approximate)  
(mucin-like domain).  
FT CARBOHYD 339 339 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 499 499 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 1216 1216 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 1239 1239 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 1314 1314 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 1814 1814 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 1908 1908 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 1933 1933 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2028 2028 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2111 2111 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2142 2142 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2332 2332 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2533 2533 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2575 2575 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2692 2692 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 2812 2812 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3052 3052 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3065 3065 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3144 3144 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3172 3172 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3288 3288 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3292 3292 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 3782 3782 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4005 4005 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4136 4136 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4243 4243 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4254 4254 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4335 4335 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4376 4376 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 4586 4586 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 5136 5136 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 5252 5252 N-linked (GlcNAc...) (Potential).  
FT DISULFID 5263 5274 By similarity.  
FT DISULFID 5268 5283 By similarity.  
FT DISULFID 5285 5294 By similarity.



SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB7DF2A2620 CRC64;

Query Match 32.1%; Score 64.5; DB 1; Length 5376;  
 Best Local Similarity 35.1%; Pred. No. 58;  
 Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIP-COLRCSNTP--PLTCQYC 34  
 Db 3300 CPTNSQFTDCLPSCVSCNRCVTSFVSSCREGC 3336

RESULT 18

Q410V5 GIBZE PRELIMINARY; PRT; 762 AA.

AC Q410V5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=PG09123.1;  
 OS Gibberella zeae PH-1.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
 OX NCBI\_TaxID=229533;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PH-1;  
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,  
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,  
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 RA Chepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,  
 RA Diaz J.S., Dodge S., Dooley K., Dorrts L., Elkins T., Engels R.,  
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,  
 RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,  
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,  
 RA Matthews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,  
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Rise C., Rogov P.,  
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Riese C., Rogov P.,  
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,  
 RA Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,  
 RA Talamas J., Teefaye S., Theodore J., Topham K., Travers M.,  
 RA Vassiliev H., Venkataranan V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 RA Lander E.;  
 RT "Fusarium graminearum genome sequence."  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; RACH01000370; EAA78173.1; -; Genomic\_DNA.  
 SQ SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;

Query Match 31.8%; Score 64; DB 2; Length 762;  
 Best Local Similarity 43.3%; Pred. No. 9.1;  
 Matches 13; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

Qy 13 ACIPQ---LRCSNTPPLTCQ-----YC 34  
 Db 17 ACVPCQNSKKRQDSQSPANCRRRDCIPYC 46

RESULT 19

Q50LY7 ENTHI PRELIMINARY; PRT; 799 AA.

AC Q50LY7;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Protein kinase, putative (Fragment).  
 GN ORFNames=650.t00003;  
 OS Entamoeba histolytica HM-1:IMSS.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_TaxID=294381;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=HM-1:IMSS;  
 RC PubMed=15729342; DOI=10.1038/nature03291;  
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuleon J.,  
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
 RA Hofer M., Bruchhaus I., Willhoef U., Hantsch B., Harris D.,  
 RA Chillingworth T., Churcher C., Hance Z., Omond D., Squares R., Whitehead S.,  
 RA Jagels K., Moule S., Mungall K., Omond D., Squares R., Whitehead S.,  
 RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
 RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,  
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
 RA Fraser C.M., Hall N.;  
 RT "The genome of the protist parasite Entamoeba histolytica."  
 RL Nature 433:865-868(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AAFB01001427; EAL42605.1; -; Genomic\_DNA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR InterPro; IPR006212; Furin repeat.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00261; FU; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT NON\_TER  
 SQ SEQUENCE 799 AA; 91662 MW; D8BPE2F2E235989E CRC64;

Query Match 31.6%; Score 63.5; DB 2; Length 799;  
 Best Local Similarity 35.3%; Pred. No. 11;  
 Matches 12; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQ---LRCSNTPPLTCQ 31  
 Db 137 CQDNYYYDKELQSCVSCSCLTCNKKDICTCK 170

RESULT 20

Q50Y51 ENTHI PRELIMINARY; PRT; 802 AA.

AC Q50Y51;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE CXXC-rich protein (Fragment).  
 GN ORFNames=141.t00017;  
 OS Entamoeba histolytica HM-1:IMSS.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_TaxID=294381;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HM-1:IMSS;  
 RC PubMed=15729342; DOI=10.1038/nature03291;

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RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moulé S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB01000471; EAL46536.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 802 AA; 90126 MW; 1425BF8514DED237 CRC64;

Query Match 31.6%; Score 63.5; DB 2; Length 802;
Best Local Similarity 35.3%; Pred. No. 11;
Matches 12; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 1 CSONEYFDSLHACIPQ---LRCSNTPPLTCQ 31
Db 654 CQNYYYKDLQSCVGCSSCLTCSNKDICTCK 697

RESULT 21
Q50PT4_ENTHI PRELIMINARY; PRT; 1150 AA.
AC Q50PT4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Receptor protein kinase, putative.
GN ORFNames=359.t00009;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS.
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moulé S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB01000933; EAL43605.1; -; Genomic_DNA.
KW Kinase; Receptor.
SQ SEQUENCE 1150 AA; 128938 MW; 0DBE7051D4B4E286 CRC64;

Query Match 31.3%; Score 63; DB 2; Length 1150;
Best Local Similarity 36.7%; Pred. No. 19;
Matches 11; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLCRSSNTPPLTC 30
Db 138 CGINEYFDVSKLNCPLCKTNCQRCSSAQC 167
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RESULT 22
Q7QGV0_ANOGA PRELIMINARY; PRT; 1294 AA.
AC Q7QGV0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000012534 (fragment).
GN ORFNames=ENSANGG00000010045;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN 2
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008823; EAA05574.2; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0008886; P:intracellular protein transport; IEA.
DR InterPro; IPR002860; Glyco_Hydro_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002172; LDL receptor A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR InterPro; IPR006581; VPS10.
DR Pfam; PF02012; BNR; 6.
DR Pfam; PF00057; Ldl_recept_a; 7.
DR Pfam; PF00058; Ldl_recept_b; 4.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00192; LDLA; 7.
DR SMART; SM00135; LY; 5.
DR SMART; SM00602; VPS10; 1.
DR PROSITE; PS01209; LDLRA_1; 5.
DR PROSITE; PS50068; LDLRA_2; 5.
FT NON TER 1
FT NON TER 1294
SQ SEQUENCE 1294 AA; 146748 MW; 10C251750A3F0586 CRC64;

Query Match 31.1%; Score 62.5; DB 2; Length 1294;
Best Local Similarity 31.7%; Pred. No. 25;
Matches 13; Conservative 8; Mismatches 13; Indels 7; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLCRSS-----NTPPLTCQRYC 34
Db 1131 CRADEFRCNVTNACLPNWRCDTEKCPDGPSTPPRRKDRTC 1171

RESULT 23
Q6BFG4_PARTE PRELIMINARY; PRT; 3005 AA.
AC Q6BFG4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative surface protein with EGF domains and furin-like repeats.
GN ORFNames=PFMB.409;
OS Paramoecium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramoecium.
```

OX NCBI\_TaxID=5888;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Stock d4-2;  
RX PubMed=15296759; DOI=10.1016/j.j.cub.2004.07.029;  
RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,  
RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Kellier A.M.,  
RA Cohen J., Meyer E., Sperling L.,  
RT "High Coding Density on the Largest Paramecium tetraurelia Somatic Chromosome."  
RL Curr. Biol. 14:1397-1404(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Stock d4-2;  
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;  
RT "Paramecium megabase sequencing project."  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR548612; CAH03606.1; -; Genomic\_DNA.  
DR InterPro; IPR006058; 2Fe2S fd BS.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR006212; Furin\_repeat.  
DR InterPro; IPR006210; IEGF.  
DR SMART; SM00181; EGF; 22.  
DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_7; 12.  
SQ SEQUENCE 3005 AA; 343821 MW; D8CC6A247876A5A5 CRC64;  
Query Match 30.6%; Score 61.5; DB 2; Length 3005;  
Best Local Similarity 40.6%; Pred. No. 80;  
Matches 13; Conservative 3; Mismatches 7; Indels 9; Gaps 2;  
QY 6 YFDSLHACIPQRCSSNTPLTCQ----RYC 34  
DB 1190 YFESSNQICDLSC-----FTCGSSKYC 1215  
RESULT 24  
ID Q22378 CABEL PRELIMINARY; PRT; 966 AA.  
AC Q22378;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein T10E10.4;  
GN ORFNames=T10E10.4;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase; WBGene00020421; T10E10.4.  
RT "The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology."  
RL Science 282:2012-2018(1998).  
DR EMBL; U39644; AAA80360.2; -; Genomic\_DNA.  
DR PIR; T16840; T16840.  
DR HSP; P10969; 1WGT.  
DR IntAct; Q22378; -.  
DR Ensembl; T10E10.4; Caenorhabditis elegans.  
DR WormBase; WBGene00020421; T10E10.4.  
DR WormPep; T10E10.4; CE25989.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0006030; P:chitin metabolism; IEA.  
DR InterPro; IPR002557; Chitin\_bind\_PeRA.  
DR InterPro; IPR006149; EB region.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000794; Ketoacyl\_synth.  
DR InterPro; IPR003571; Snake\_toxin.

DR InterPro; IPR006150; Worm\_repeat\_1.  
DR Pfam; PF01607; CBM\_14; 2.  
DR Pfam; PF01683; EB; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00289; WRI; 12.  
DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; UNKNOWN\_1.  
DR PROSITE; PS00272; SNAKE\_TOXIN; UNKNOWN\_1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 966 AA; 102461 MW; B565A3CDD25216D9 CRC64;  
Query Match 30.3%; Score 61; DB 2; Length 966;  
Best Local Similarity 37.5%; Pred. No. 29;  
Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;  
QY 1 CSQNEVFDSLHACIPQCLR--CSSNTPLTC 30  
DB 216 CSQSTFVNSDLNVCVPLATQNSDSSTQQPVC 247  
RESULT 25  
ID Q5JSG7 HUMAN PRELIMINARY; PRT; 1560 AA.  
AC Q5JSG7;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Protease convertase subtilisin/kexin type 5 (Fragment).  
GN Name=PCSK5; ORFNames=RP11-422N19.4-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Mashreghi-Mohammadi M.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Pelan S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Peck A.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL391868; CA140675.1; -; Genomic\_DNA.  
DR EMBL; AL589653; CA140809.1; -; Genomic\_DNA.  
DR EMBL; AL353607; CA140675.1; JOINED; Genomic\_DNA.  
DR EMBL; AL353607; CA140675.1; JOINED; Genomic\_DNA.  
DR EMBL; AL353607; CA140809.1; JOINED; Genomic\_DNA.  
DR EMBL; AL589653; CA140675.1; JOINED; Genomic\_DNA.  
DR EMBL; AL391868; CA140809.1; JOINED; Genomic\_DNA.  
DR EMBL; AL391868; CA141234.1; JOINED; Genomic\_DNA.  
DR EMBL; AL589653; CA141234.1; JOINED; Genomic\_DNA.  
DR GO; GO:0004289; F:subtilase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR003460; APP.  
DR InterPro; IPR005560; DUF326.  
DR InterPro; IPR006212; Furin\_repeat.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000209; Pept\_S8\_S53.  
DR InterPro; IPR002884; PrprotnconvertP.  
DR Pfam; PF02420; AFP; 1.  
DR Pfam; PF03860; DUF326; 2.  
DR Pfam; PF01483; P\_proproteain; 1.  
DR ProDom; PD000717; PrprotnconvertP; 1.  
DR SMART; SM00181; EGF; 16.  
DR SMART; SM00261; FU; 22.  
DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
FT NON TER 1  
SQ SEQUENCE 1560 AA; 173890 MW; 7211FBC127A8A08C CRC64;  
Query Match 30.3%; Score 61; DB 2; Length 1560;

**Qy**      1 CSQNEYFDLLHACI-----PQLRCSSNTTPL-----TCORYC 34  
      ||| ||| :: | :| | | | :|||  
**Db**     144 CSVNSICDAMTGRLCSPGWTRNGCIQCNNSPDOFTGRCCRERLWGPRCEY C 201

FT	DOMAIN	245	304		WFCC.
FT	DOMAIN	344	502		F5/8 type C.
FT	DOMAIN	506	544		LDL-receptor class A 1.
FT	DOMAIN	663	701		LDL-receptor class A 2.
FT	DOMAIN	723	761		LDL-receptor class A 3.
FT	DOMAIN	761	814		TSP type-1 3.
FT	DOMAIN	816	866		TSP type-1 4.
FT	CARBOHYD	88	88		N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD	309	309		N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD	409	409		N-linked (GLCNAC. .) (Potential).
FT	DISULFID	107	122		By similarity.
FT	DISULFID	116	127		By similarity.
FT	DISULFID	129	141		By similarity.
FT	DISULFID	147	166		By similarity.
FT	DISULFID	149	169		By similarity.
FT	DISULFID	171	179		By similarity.
FT	DISULFID	344	502		By similarity.
FT	DISULFID	508	520		By similarity.
FT	DISULFID	515	533		By similarity.
FT	DISULFID	527	542		By similarity.
FT	DISULFID	665	677		By similarity.
FT	DISULFID	672	690		By similarity.
FT	DISULFID	684	699		By similarity.
FT	DISULFID	725	737		By similarity.
FT	DISULFID	732	750		By similarity.
FT	DISULFID	744	759		By similarity.
FT	NON_TER	1	1		
FT	NON_TER	867	867		
SQ	SEQUENCE	867 AA;	91817 MW;	9538F2108E787B49 CRC64;	
 Query Match 29.9%; Score 60; DB 1; Length 867; Best Local Similarity 42.9%; Pred. No. 35; Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;					
Qy	10 LLHACIPCOLRCSSTNPPLTC 30 :     : :				
Db	96 VFHACVCPCLTCDDISQATC 116 :     : :				
 RESULT 28					
ID	Q8SPM4_BOVIN				
ID	Q8SPM4_BOVIN PRELIMINARY;	PRT;	5146 AA.		
AC	Q8SPM4;				
DT	01-JUN-2002 (TrEMBLrel. 21, Created)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	SCO-spondin.				
GN	Name=sco-spondin;				
OS	Bos taurus (Bovine);				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;				
OC	Pecora; Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Subcommissural organ;				
EX	MEDLINE=20465125; PubMed=11008217;				
RX	DOI=10.1002/1098-1136(200011)32:2<177::AID-GLIA70>3.0.CO;2-V;				
RA	Gobron S.;				
RT	"Subcommissural organ/Reissner's fiber complex: characterization of				
RT	sco-spondin, a glycoprotein with potent activity on neurite				
RT	outgrowth.";				
RL	Glia 32:177-191(2000).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Subcommissural organ;				
RA	Meinzel A.;				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AJ416457; CAC94914.1; -; mRNA.				
DR	HSSP; P98162; 1K7B.				
DR	GO; GO:0005576; C:extracellular region; IEA.				
DR	GO; GO:0005179; F:hormone activity; IEA.				
DR	GO; GO:0030414; F:protease inhibitor activity; IEA.				

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RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071103; AAU48725.1; -; mRNA.
DR Ensembl; CG7348; Drosophila melanogaster.
DR FlyBase; FBgn0036940; CG7348.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM 14; 4.
DR SMART; SM00494; ChitBD2; 3.
DR PROSITE; PS50940; CHIT BIND II; 4.
SQ SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FP9921 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

QY 1 CSQNEVFDLSLLHACIPCOL-----RCSNTP-----PLTCQRY 33
Db 119 CSVGNYPDPARRACLPVAISAAHQSCVLPDNATLANPDSCEY 162

RESULT 30
Q9VW81.DROME
ID Q9VW81.DROME PRELIMINARY; PRT; 353 AA.
AC Q9VW81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG7348-PA.
GN Name=CG7348; ORFNames=CG7348;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mankov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleby J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Stadling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleby J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleby J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003514; AAF49068.1; -; Genomic DNA.
DR Ensembl; CG7348; Drosophila melanogaster.
DR FlyBase; FBgn0036940; CG7348.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM 14; 4.
DR SMART; SM00494; ChitBD2; 3.
DR PROSITE; PS50940; CHIT BIND II; 4.
SQ SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

QY 1 CSQNEVFDLSLLHACIPCOL-----RCSNTP-----PLTCQRY 33
Db 119 CSVGNYPDPARRACLPVAISAAHQSCVLPDNATLANPDSCEY 162

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RESULT 31
Q5CZ68 HUMAN PRELIMINARY; PRT; 484 AA.
AC Q5CZ68;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686D20108 (Fragment).
GN Name=DKFZp686D20108;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RG Tissue=Fetal kidney;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR936873; CAI59785.1; -.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 484 AA; 53895 MW; 8895A663B9DB369C CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 484;
Best Local Similarity 28.9%; Pred. No. 22;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOL-----RCSNT 25
|||:::|||||:
Db 241 CSPGHYNTSIHRCAMGYSQPDFRNFCSRCPGNT 278

RESULT 32
Q8NAV8 HUMAN PRELIMINARY; PRT; 581 AA.
AC Q8NAV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ34691.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura N., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima N., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

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RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45 (2004).
DR EMBL; AK092010; BAC03789.1; -. mRNA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4EE1 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 581;
Best Local Similarity 28.9%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOL-----RCSNT 25
|||:::|||||:
Db 337 CSPGHYNTSIHRCAMGYSQPDFRNFCSRCPGNT 374

RESULT 33
Q5CZB3 HUMAN PRELIMINARY; PRT; 852 AA.
AC Q5CZB3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686B1223 (Fragment).
GN Name=DKFZp686B1223;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR936607; CAI56752.1; -. mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0007536; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001491; Thrombomoduln.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00042; CUB; 1.

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DR SMART; SM00181; EGF; 7.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
KW EGF-like domain; Hypothetical protein.
FT NON_TER
SQ SEQUENCE 852 AA; 93812 MW; 514918C0DD126C7B2 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 852;
Best Local Similarity 28.9%; Pred. No. 40;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPQL-----RCSNNT 25
|||:::|||||
Db 608 CSPGHYNTSIHRCIRCAMGSPQDFRQNFCSRCPGNT 645

RESULT 34
Q55NL5_CRYNE PRELIMINARY; PRT; 861 AA.
AC Q55NL5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNAMES=CNBH0730;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiellia.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary.
DR EMBL; AA0Y0100041; EAL19380.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 93346 MW; 8745729FBD869366 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 861;
Best Local Similarity 37.1%; Pred. No. 40;
Matches 13; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTPP-----LTC 30
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Db 321 CSSGLYYDSTSSCSPACSTCTGPTGDSCLSC 355

RESULT 35
Q8NAU9_HUMAN PRELIMINARY; PRT; 880 AA.
ID Q8NAU9_HUMAN PRELIMINARY;
AC Q8NAU9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ34743.
GN Name=SCUBE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;

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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa K., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togai S., Komai F., Hara R., Takeuchi K., Arica M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inegaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Negase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Iwogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK092062; BAC03798.1; -; mRNA.
DR HSSP; P35555; ILMJ.
DR Ensembl; ENSG00000146197; Homo sapiens.
DR HGNC; HGNC:13655; SCUBE3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 2.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR PRINTS; PR00907; THRBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
SQ SEQUENCE 880 AA; 97239 MW; F0BDE6E85266FD60 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 880;
Best Local Similarity 28.9%; Pred. No. 41;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPQL-----RCSNNT 25
|||:::|||||
Db 636 CSPGHYNTSIHRCIRCAMGSPQDFRQNFCSRCPGNT 673

RESULT 36
Q8IZ06_HUMAN PRELIMINARY; PRT; 985 AA.
ID Q8IZ06_HUMAN PRELIMINARY;
AC Q8IZ06;

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DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC26979 protein.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032835; AAH32835.1; -; mRNA.
DR Ensembl; ENSG00000164953; Homo sapiens.
DR InterPro; IPR000150; Hypothet cof.
DR PROSITE; PS01228; COF_1; UNKNOWN_1.
SQ SEQUENCE 985 AA; 110872 MW; 971B5626C726B384 CRC64;
Query Match 29.6%; Score 59.5; DB 2; Length 985;
Best Local Similarity 21.6%; Pred. No. 46;
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;

Qy 1 CSQNEYFDSLHACIPC-----QLRCSNTPPLTCQR 32
Db 39 CDNNQYFDISALSCVPCGANQRDARGTSCVCLPGFQMISNNGGPAIICKK 89

RESULT 37
Q725T8 HUMAN
ID Q725T8 HUMAN PRELIMINARY; PRT; 985 AA.
AC Q725T8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC26979.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032835; AAH32835.1; -; mRNA.
DR Ensembl; ENSG00000164953; Homo sapiens.
DR InterPro; IPR000150; Hypothet cof.
DR PROSITE; PS01228; COF_1; UNKNOWN_1.
SQ SEQUENCE 985 AA; 110872 MW; 971B5626C726B384 CRC64;
Query Match 29.6%; Score 59.5; DB 2; Length 985;
Best Local Similarity 21.6%; Pred. No. 46;
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;

Qy 1 CSQNEYFDSLHACIPC-----QLRCSNTPPLTCQR 32
Db 39 CDNNQYFDISALSCVPCGANQRDARGTSCVCLPGFQMISNNGGPAIICKK 89

RESULT 37
Q725T8 HUMAN
ID Q725T8 HUMAN PRELIMINARY; PRT; 985 AA.
AC Q725T8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC26979.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054338; AAH54338.1; -; mRNA.
DR InterPro; IPR000150; Hypothet cof.
DR PROSITE; PS01228; COF_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 985 AA; 110858 MW; 711109F095C12E89 CRC64;
Query Match 29.6%; Score 59.5; DB 2; Length 985;
Best Local Similarity 21.6%; Pred. No. 46;
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;

Qy 1 CSQNEYFDSLHACIPC-----QLRCSNTPPLTCQR 32
Db 39 CDNNQYFDISALSCVPCGANQRDARGTSCVCLPGFQMISNNGGPAIICKK 89

RESULT 38
Q86U29 HUMAN
ID Q86U29 HUMAN PRELIMINARY; PRT; 992 AA.
AC Q86U29;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Signal peptide, CUB domain, EGF-like 3.
GN Name=SCUBE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";   
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RA Strauberg R.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC052263; AAHS2263.2; -; mRNA.  
DR HSSP; P35555; 1EMN.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR000152; Aex hydroxyl_s.  
DR InterPro; IPR000859; CUB_2.  
DR InterPro; IPR000742; EGF_2.  
DR InterPro; IPR001881; EGF_Ca.  
DR InterPro; IPR006209; EGF_Like.  
DR InterPro; IPR011641; GCC2_GCC3.  
DR InterPro; IPR006210; IBGF.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF_CA; 4.  
DR Pfam; PF07699; GCC2_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 10.  
DR SMART; SM00179; EGF_CA; 7.  
DR PROSITE; PS00010; ASX_HYDROXYL; 6.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF_2; 7.  
DR PROSITE; PS50026; EGF_3; 6.  
DR PROSITE; PS01187; EGF_CA; 6.  
SQ SEQUENCE 992 AA; 109165 MW; 24093050738932E1 CRC64;  
  
Query Match 29.6%; Score 59.5; DB 2; Length 992;  
Best Local Similarity 28.9%; Pred. No. 47;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPCOL-----RCSST 25  
Db 748 CSPGHYYNTSIHRCIRCAMGSYQDPFRQNFCSRCPGNT 785  
  
RESULT 39  
Q8IX30_HUMAN PRELIMINARY; PRT; 993 AA.  
AC Q8IX30;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE CUB and EGF containing protein (Signal peptide, CUB and EGF-like  
DE domain containing protein 3 precursor) (OPTHUMP00000016250).  
GN Name=SCUBE3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R.,  
RA Hankeln T., Winterpacht A.;  
RT "Novel human gene family (CEGF) encoding mosaic proteins with EGF-  
RT like, SVT2R and a CUB module: cloning and expression analysis.";   
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RX PubMed=15234972; DOI=10.1074/jbc.M405912200;  
RA Wu B.T., Su Y.H., Tsai M.T., Wasserman S.M., Topper J.N., Yang R.B.;  
RT "A novel secreted, cell-surface glycoprotein containing multiple  
RT epidermal growth factor-like repeats and one CUB domain is highly  
RT expressed in primary osteoblasts and bones.";   
RL J. Biol. Chem. 279:37485-37490(2004).  
[3]  
  
RP NUCLEOTIDE SEQUENCE.  
RA Williams S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF452494; AAN76808.1; -; mRNA.  
DR EMBL; AY639608; AAU08347.1; -; mRNA.  
DR EMBL; Z97832; CAI20187.1; -; Genomic_DNA.  
DR HSSP; P35555; 1EMN.  
DR Ensembl; ENSG00000146197; Homo sapiens.  
DR HGNC; HGNC:13655; SCUBE3.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR000152; Asx hydroxyl_s.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF_2.  
DR InterPro; IPR001881; EGF_Ca.  
DR InterPro; IPR006209; EGF_Like.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 6.  
DR Pfam; PF07645; EGF_CA; 3.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00179; EGF_CA; 6.  
DR PROSITE; PS00010; ASX_HYDROXYL; 6.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF_2; 7.  
DR PROSITE; PS50026; EGF_3; 6.  
DR PROSITE; PS01187; EGF_CA; 6.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 993 AA; 109282 MW; 19BBE0E5627EEAF4 CRC64;  
  
Query Match 29.6%; Score 59.5; DB 2; Length 993;  
Best Local Similarity 28.9%; Pred. No. 47;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPCOL-----RCSST 25  
Db 749 CSPGHYYNTSIHRCIRCAMGSYQDPFRQNFCSRCPGNT 786  
  
RESULT 40  
QSHYA8_HUMAN PRELIMINARY; PRT; 995 AA.  
AC QSHYA8;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein DKFZp686F1937.  
GN Name=DKFZp686F1937;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
RA Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX648768; CAI45999.1; -; mRNA.  
DR InterPro; IPR000150; Hypothet_cof.  
DR PROSITE; PS01228; COF_1; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 995 AA; 111730 MW; AEBD4A6B84F759A8 CRC64;  
  
Query Match 29.6%; Score 59.5; DB 2; Length 995;  
Best Local Similarity 21.6%; Pred. No. 47;  
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPCL-----QLRCSSTNPPLTCQR 32
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Db 49 CDNNQYFDISALSCVPCGANQRQDARGTSCVCLPGFQMSNNGGPAICCK 99
RESULT 41
Q4S403_TETNG
ID Q4S403_TETNG PRELIMINARY; PRT; 184 AA.
AC Q4S403
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAP14738, whole genome shotgun sequence.
GN ORFNames=CSTENG0024082001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAE01014738; CAG04379.1; -: Genomic DNA.
SQ SEQUENCE 184 AA; 19133 MW; 3B2167E5E4FB1BB7 CRC64;
Query Match 29.4%; Score 59; DB 2; Length 184;
Best Local Similarity 27.3%; Pred. No. 9;
Matches 9; Conservative 10; Mismatches 4; Indels 10; Gaps 1;
QY 1 CSQNEYFDLSLHACIPQCLRSSNTPLTCQRY 33
Db 94 CSSEFWNSVDVCPCE-----SCKKY 116
RESULT 42
Q9GYR5_CABEL
ID Q9GYR5_CABEL PRELIMINARY; PRT; 937 AA.
AC Q9GYR5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C23G10.8.
GN ORFNames=C23G10.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
Science 282:2012-2018(1998).
CC -!- INTERACTION:
CC Q4S080:Cl7H12.9; NbExp=1; IntAct=EBI-312175, EBI-312180;
CC F41829:nhr-6; NbExp=1; IntAct=EBI-312175, EBI-314469;
CC EMBL; U39851; AAF99879.1; -: Genomic_DNA.
DR PIR; T15577; T15577.
DR IntAct; Q9GYR5; -.
DR Ensembl; C23G10.8; Caenorhabditis elegans.
DR WormBase; WSGene00016015; C23G10.8.
DR WormFep; C23G10.8; CE25784.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 937 AA; 106669 MW; 1C140595DFD3ACE4 CRC64;
Query Match 29.4%; Score 59; DB 2; Length 937;
Best Local Similarity 42.9%; Pred. No. 51;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 8 DSLHACIPQCLRSSNTPL 28
Db 439 ESVFHPLYPAEIRCSADGPPL 459
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RESULT 43
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ID Q51ED6_ENTHI PRELIMINARY; PRT; 1917 AA.
AC Q51ED6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protein kinase, putative.
GN ORFNames=10.t00040;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=1579342; DOI=10.1038/nature03291;
RA Lotus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitz E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichevitz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB0100051; EAL51211.1; -: Genomic_DNA.
DR GO; GO:0016301; P.kinase activity; IEA.
DR InterPro; IPR012286; Pcc3_N_cyt.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR004094; Prot_inh_antistn.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF02822; Anticasin; 1.
DR Pfam; PF07699; GCC2_GCC3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00181; EGF; 11.
```

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalao D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y., Schein J.Z., Krzywinski M.I., Skaleka U., Smillius D.E., Schnerch A., Shen J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC079849; AAH79849.1; -; mRNA.  
MGI; MGI:3045253; Scube3.  
GO; GO:0005509; F.calcium ion binding; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF\_CA; 3.  
DR Pfam; PF07699; GCC2\_GCC3; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 9.  
DR SMART; SM00179; EGF\_CA; 7.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
DR PROSITE; PS01180; CUB\_1.  
DR PROSITE; PS01186; EGF\_2; 6.  
DR PROSITE; PS00026; EGF\_3; 4.  
DR PROSITE; PS01187; EGF\_CA; 4.  
KW EGF-like domain.  
FT NON TER 1 1  
SQ SEQUENCE 827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;

Query Match 29.1%; Score 58.5; DB 2; Length 827;  
Best Local Similarity 28.9%; Pred. No. 53;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
QY 1 CSQNEYFDLSLLHACIPCOL-----RCSNNT 25  
Db 611 CSPGHVYNTSIHRCAVGSGYPDFRQNFCRCPGNT 648  
|:::|||||:  
|||

RESULT 46  
Q66PY1\_MOUSE PRELIMINARY; PRT; 993 AA.  
ID Q66PY1\_MOUSE PRELIMINARY;  
AC Q66PY1;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Signal peptide, CUB and EGF-like domain containing protein 3 precursor.  
DE precursor.  
GN Name=Scube3; Synonyms=SCUBE3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6;  
RX PubMed=15234972; DOI=10.1074/jbc.M405912200; Topper J.N., Yang R.B.;  
RA Wu B.F., Su Y.H., Tsai M.T., Wasserman S.M., 1999; 1;  
RT "A novel secreted, cell-surface glycoprotein containing multiple  
RT epidermal growth factor-like repeats and one CUB domain is highly  
RT expressed in primary osteoblasts and bones.";  
RL J. Biol. Chem. 279.37485-37490 (2004).  
DR EMBL; AY339609; AAU08348.1; -; mRNA.  
DR MGI; MGI:3045253; Scube3.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR00152; ASX hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR00742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF\_CA; 4.  
DR Pfam; PF07699; GCC2\_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 10.  
DR SMART; SM00179; EGF\_CA; 8.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 6.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS00026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 6.  
KW Signal.  
FT SIGNAL 1 28 Potential.  
SQ SEQUENCE 993 AA; 108983 MW; E43989ACACCC345F CRC64;  
Query Match 29.1%; Score 58.5; DB 2; Length 993;  
Best Local Similarity 28.9%; Pred. No. 63;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
Qy 1 CSQNEYFDLLHACIPQL-----RCSSNT 25  
Db 749 CSPGHYNTSIHRCVAGSYQDPFRQNFCTRCPGNT 786  
RESULT 47  
Q8BR19\_MOUSE PRELIMINARY; PRT; 101 AA.  
AC Q8BR19;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length  
DE enriched library, clone:B230316E19 product:hypothetical protein, full  
DE insert sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RX Carninci P., Hayashizaki Y.;  
RA "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44 (1999).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fushimi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RX Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bares G.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohleuli S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RC The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
[4]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
[5]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
[6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kigawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK045875; BAC32518.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 101 AA; 11571 MW; E899420B6F215D23 CRC64;  
Query Match 28.9%; Score 58; DB 2; Length 101;  
Best Local Similarity 31.9%; Pred. No. 7.1;  
Matches 15; Conservative 5; Mismatches 9; Indels 18; Gaps 2;  
Qy 6 YFSLHACIPPC-----QRCSSNTTP-----LTCQRYC 34  
Db 4 YFNSLLFLFCFKRLTLRLCTSHPPPPPPPPPPPPSHSLACGYC 50



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RESULT 51
Q26489_SPOFR Q26489_SPOFR PRELIMINARY; PRT; 1299 AA.
ID ID Q26489_SPOFR PRELIMINARY; PRT; 1299 AA.
AC AC Q26489;
DT DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE DE Endoprotease FURIN.
GN GN Names:FURIN;
OS OS Spodoptera frugiperda (Fall armyworm).
OC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC OC Noctuidae; Amphipyrinae; Spodoptera.
OX OX NCBI_TaxID=7108;
RN RN [1]
RP RP NUCLEOTIDE SEQUENCE.
RC RC TISSUE=Sf9;
RA RA Cleplik M., Klenk H.;
RL RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR DR EMBL; Z88888; CAA33116.1; -, mRNA.
DR DR PIR; T43251; T43251.
DR DR HSSP; P23188; 1P8J.
DR DR GO; GO:0016020; C:membrane; IEA.
DR DR GO; GO:0005524; F:ATP binding; IEA.
DR DR GO; GO:0008233; F:peptidase activity; IEA.
DR DR GO; GO:0004289; F:subtilase activity; IEA.
DR DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . ; IEA.
DR DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.
DR DR InterPro; IPR006212; Furin_repeat.
DR DR InterPro; IPR000209; Pept_S8_S53.
DR DR InterPro; IPR002884; ProtnconvertSP.
DR DR Pfam; PF01483; P_proprotein; 1.
DR DR Pfam; PF00082; Peptidase_S8; 1.
DR DR PRINTS; PR00723; SUBTILISIN.
DR DR SMART; SMO0261; FU; 10.
DR DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW KW Protease.
SQ SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;

Query Match 28.9%; Score 58; DB 2; Length 1299;
Best Local Similarity 37.1%; Pred.No. 97;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps

Oy 1 CSQNEVFDSLHACIPQLRCS-----SNTPLPTC 30
||| ||| ||| ||| ||| :||| |
Db 1150 CSRPLRIDRLNNQCVC---CSERGVTNSTPPPTDC 1181

RESULT 52
ICEI_ASCSU ICEI_ASCSU STANDARD; PRT; 63 AA.
AC AC P07851; O77419;
DT DT 01-AUG-1988 (Rel. 08, Created)
DT DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE DE Chymotrypsin/elastase isoform 1 (C/E-1 inhibitor) (ASC/E-1).
OS OS Ascaris suum (Pig roundworm) (Ascaris lumbricoideus).
OC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC OC Ascaridae; Ascaris.
OX OX NCBI_TaxID=6253;
RN RN [1]
RP RP PROTEIN SEQUENCE.
RA RA MEDLINE=84255715; PubMed=6564898;
RX RX Babin D.R., Peanasky R.J., Goos S.M.;
RT RT "The isoforms of chymotrypsin/elastase from Ascaris lumbricoideus:
the primary structure.";
RL Arch. Biochem. Biophys. 232:143-161(1984).
RN RN [2]
RP RP NUCLEOTIDE SEQUENCE.
```

```

RX MEDLINE=98297373; PubMed=9635450; DOI=10.1006/expr.1998.4284;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RT "Anisakis simplex: mutational bursts in the reactive site centers of
RL serine protease inhibitors from an ascarid nematode.";
RN Exp. Parasitol. 89:257-261(1998).
RP [3]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
RA MEDLINE=95006335; PubMed=7922044;
RA Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
RT "The molecular structure of the complex of Ascaris
RL chymotrypsin/elastase inhibitor with porcine elastase.";
RN Structure 2:679-689(1994).
CC -|- FUNCTION: Defends the organism against the host's proteinases.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Contains 1 TIL (trypsin inhibitory-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U94499; AAC61300.1; -; mRNA.
CC PDB; 1EAI; X-ray; C/D=1-61.
CC InterPro; IPR002919; Prot_Inh_CR_TIL.
CC Pfam; PF01826; TIL; 1.
KW 3D-structure; Direct protein sequencing; Protease inhibitor;
FT Serine protease inhibitor.
FT DOMAIN 5 60 TIL.
FT SITE 31 32 Reactive bond.
FT DISULFID 5 38
FT DISULFID 14 33
FT DISULFID 17 29
FT DISULFID 21 60
FT DISULFID 40 54
FT CONFLICT 4 4
FT CONFLICT 23 24 S -> R (in Ref. 2).
FT TURN 3 4 PD -> DP (in Ref. 2).
FT TURN 7 8
FT STRAND 10 12
FT STRAND 15 15
FT STRAND 20 20
FT TURN 25 26
FT STRAND 28 30
FT STRAND 34 34
FT STRAND 37 39
FT HELIX 42 44
FT TURN 45 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 54 56
FT HELIX 57 59
SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;

Query Match 28.6%; Score 57.5; DB 1; Length 63;
Best Local Similarity 37.1%; Pred. No. 5.1;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

QY 1 CSQNEYFDSLHACIPQLRC--SSNTP-PLTCOR 32
Db | | | | | | | | | | | | | | | | |
5 CGNEVWTE---CTGCEMKGGPDNTPCPLMCR 35

RESULT 53
Q5BI10 DROME PRELIMINARY; PRT; 1061 AA.
AC Q5BI10;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LD05524p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
```

```

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Friese E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021414; AAX33562.1; -; mRNA.
DR InterPro; IPR010980; Cyt_c_b562.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR012286; Fc3 N cyt.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR011025; GproteinA_insert.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR010503; LT-11B.
DR InterPro; IPR002186; NCS-type chromop.
DR InterPro; IPR000070; Pectinesterase.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR004094; Prot_inh_antistn.
DR InterPro; IPR002884; Ppirtcnconvertsp.
DR InterPro; IPR008919; Retrov_capsid_N.
DR Pfam; PF01483; P_protein; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
DR SEQUENCE 1061 AA; 115699 MW; 4E71FC5388FF229 CRC64;

Query Match 28.6%; Score 57.5; DB 2; Length 1061;
Best Local Similarity 34.3%; Pred. No. 92;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSS-NTPPLTCORYC 34
Db |||::: | | | | | | | | | | | | |
580 CSESEFYSQVQGRPCPCASCGSCNGPADTCTSC 614

RESULT 54
FUR2 DROME
ID FUR2 DROME STANDARD; PRT; 1679 AA.
AC P30432; Q24301; Q8SZS2;
DT 01-APR-1993 (Rel. 25, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin-2).
GN Name=Fur2; ORFNames=CG18734;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM D).
RC STRAIN=Iso-1; Oregon-R, and Tuebingen;
RX MEDLINE=92381036; PubMed=1512259;
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dunke U.,
RA Roebroek A.J.M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
RT "Cloning and functional expression of Dfurin2, a subtilisin-like
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RL J. Biol. Chem. 267:17208-17215(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM D).
RC STRAIN=Iso-1;
RX MEDLINE=95186060; PubMed=7880443;
RA Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
RA van de Ven W.J.M.;
RT "The Dfur2 gene of Drosophila melanogaster: genetic organization,
RT expression during embryogenesis, and pro-protein processing activity
RT of its translational product Dfurin2.";
RL DNA Cell Biol. 14:223-234(1995).
```



[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=Berkeley; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDLINE=20196006;

Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaskey E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de la Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista A.C., Ferraz C., Ferrier S., Fleischmann W., Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K., Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jallali B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Nusskern D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000).

[4] GENOME REANNOTATION, AND ALTERNATIVE SPLICING.

MEDLINE=22426069; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochkin S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review." Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).

[5] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 305-1679 (ISOFORM A).

STRAIN=Berkeley; TISSUE=Embryo; MEDLINE=22426066; PubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacle J.M., Park S., Wan K.H., Rubin G.M., Celisner S.E.; "A *Drosophila* full-length cDNA resource." Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

-1- FUNCTION: Furin is likely to represent the ubiquitous endoprotease activity within constitutive secretory pathways and capable of cleavage at the RX(K/R)R consensus motif (By similarity).

-1- CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their respective precursors.

-1- INTERACTION:

Q9W4G3:CG15470; NBExp=1; IntAct=EBI-496684, EBI-162037; Q94524:DIC90F; NBExp=1; IntAct=EBI-496684, EBI-158251; -1- ALTERNATIVE PRODUCTS;

Name=D; Synonyms=E; Name=A; Synonyms=B; IsoId=P30432-1; Sequence=Displayed; IsoId=P30432-2; Sequence=VSP\_009365;

NOTE=No experimental confirmation available;

-1- TISSUE SPECIFICITY: Transient expression in a subset of central nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic development.

-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.

-1- SIMILARITY: Belongs to the peptidase S8 family, Furin subfamily.

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EMBL; M94375; AAA28551.1; --; mRNA.

EMBL; L33831; AAA69660.1; --; Genomic DNA.

EMBL; AE003502; AAF48598.2; --; Genomic DNA.

EMBL; AE003502; AAN09400.1; --; Genomic DNA.

EMBL; AY070553; AAL48024.1; ALT\_INIT; mRNA.

PIR; A43434; A43434.

HSP; P21188; I18J.

INTACT; P30432; --.

MEROPS; S08.049; --.

Ensembl; CG18734; Drosophila melanogaster.

FlyBase; FBgn004598; Fur2.

GO; GO:0004276; F.furin activity; IDA.

InterPro; IPR006212; Furin\_repeat.

InterPro; IPR006210; IEGF.

InterPro; IPR00209; Pept\_S8\_S53.

InterPro; IPR002884; PrptnconvertP.

Pfam; PF01483; P.protein; 2.

Pfam; PF00082; Peptidase\_S8; 1.

PRINTS; PR00723; SUBTILISIN.

ProDom; PD000717; PrptnconvertP; 1.

SMART; SM00181; EGF; 1.

SMART; SM00261; FU; 10.

PROSITE; PS00136; SUBTILASE\_HIS; 1.

PROSITE; PS00137; SUBTILASE\_SER; 1.

PROSITE; PS00138; SUBTILASE\_SER; 1.

Alternative splicing; Glycoprotein; Hydrolase; Multigene family; Protease; Repeat; Serine protease; Signal; Transmembrane; Zymogen.

SIGNAL 1 ? Potential.

PROPEP 1 318 Potential.

CHAIN 319 1679 Furin-like protease 2.

TRANSMEM 1512 1532 Potential.

TOPO\_DOM 1533 1679 Cytoplasmic (Potential).

REPEAT 961 1006 1.

REPEAT 1007 1056 2.

REPEAT 1057 1103 3.

REPEAT 1104 1152 4.

REPEAT 1153 1204 5.

REPEAT 1205 1253 6.

REPEAT 1254 1298 7.

REPEAT 1299 1345 8.

REPEAT 1346 1392 9.

REPEAT 1393 1443 10.

REGION 961 1443 10 X tandem repeats, Cys-rich.

ACT\_SITE 417 417 Charge relay system (By similarity).

ACT\_SITE 456 456 Charge relay system (By similarity).

ACT\_SITE 637 637 Charge relay system (By similarity).

CARBOHYD 3 N-linked (GlcNAc...) (Potential).

CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).

CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).

CARBOHYD 205 205 N-linked (GlcNAc...) (Potential).

CARBOHYD 442 442 N-linked (GlcNAc...) (Potential).



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DR GO: 0008061; F:chitin binding; IEA.
DR GO: 0006030; P:chitin metabolism; IEA.
DR InterPro: IPR002557; Chitin_bind_PeA.
DR InterPro: IPR006149; EB_region.
DR InterPro: IPR000794; Ketoacyl_synth.
DR InterPro: IPR003571; Snake_toxin.
DR Pfam: PF01607; CBM_14; 2.
DR Pfam: PF01683; EB; 1.14.
DR SMART; SMO0289; WRI; 14.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 919 AA; 96816 MW; B33EFC096CE53DFD CRC64;

Query Match 28.4%; Score 57; DB 2; Length 919;
Best Local Similarity 34.4%; Pred. No. 92;
Matches 11; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHLHACIPQLR--CSNTPTPLTC 30
Db 164 CSQSTVFNAELSCVCLAIQNSCDSTQQPVC 195

RESULT 58
Q7R165 GIALA
ID Q7R165 GIALA PRELIMINARY; PRT; 1210 AA.
AC Q7R165;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_447-61408.57776.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OC NCBI_TaxID=184922;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G.; McArthur A.G.; Adam R.D.; Alley S.B.; Gillin F.D.;
RA Olsen G.J.; Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000029; EAA41074.1; -; Genomic_DNA.
DR HSSP; P25963; 1IKN.
DR InterPro: IPR002110; ANK.
DR Pfam; PF00023; Ank; 20.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 2.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR ANK repeat; Repeat.
SQ SEQUENCE 1210 AA; 132501 MW; 0AC83EEA78A5D726 CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1210;
Best Local Similarity 35.7%; Pred. No. 1.2e+02;
Matches 15; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

Qy 1 CSQNEYFDSLHLH-----ACIPC-----QLRCSSNTPTPL 28
Db 549 CIRNNGYDTHALHIAVASKSFACIPCLAAVEAIRDSHNRNAL 590

RESULT 59
Q26566 SCHMA
ID Q26566 SCHMA PRELIMINARY; PRT; 1717 AA.
AC Q26566;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epidermal growth factor receptor precursor.
GN Name=SER;

OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Puerto Rican;
RC MEDLINE=92365727; PubMed=1501637; DOI=10.1016/0166-6851(92)90003-3;
RA Shoemaker C.B.; Ramachandran H.; Landa A.; dos Reis M.G.; Stein L.;
RT "Alternative splicing of the Schistosoma mansoni gene encoding a
RT homologue of epidermal growth factor receptor.";
RL Mol. Biochem. Parasitol. 53:17-32(1992).
DR EMBL; M86396; AAA29866.1; -; mRNA.
DR PIR; A45558; A45558.
DR HSSP; P11362; IFGK.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0005224; F:ATP binding; IEA.
DR GO: 0005006; F:epidermal growth factor receptor activity; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR GO: 0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR InterPro: IPR000494; EGFR_L.
DR InterPro: IPR006211; Furin-like.
DR InterPro: IPR006212; Furin repeat.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam; PF00757; Furin-like; 2.
DR Pfam; PF01030; Recep_L domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SMO0261; FU; 6.
DR SMART; SMO0219; Tyrc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1 19 potential.
FT CHAIN 20 1717 epidermal growth factor receptor.
SQ SEQUENCE 1717 AA; 192303 MW; 1101A338C1653D8C CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1717;
Best Local Similarity 40.9%; Pred. No. 1.8e+02;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHLHACIPQLRCS 22
Db 646 CPRNTYIDPQTRHCLPCNCS 667

RESULT 60
Q8WRF4 MONBE
ID Q8WRF4 MONBE PRELIMINARY; PRT; 1476 AA.
AC Q8WRF4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Receptor tyrosine kinase.
GN Name=MBRTK1;
OS Monosiga brevicollis.
OC Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.
OX NCBI_TaxID=81824;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 50154;
RC MEDLINE=21625102; PubMed=11752452; DOI=10.1073/pnas.261477698;
RA King N.; Carroll S.B.;
RT "A receptor tyrosine kinase from choanoflagellates: molecular insights
RT into early animal evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15032-15037(2001).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 50154;
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RX MEDLINE=22752269; PubMed=12869759; DOI=10.1126/science.1083853;
RA King N., Hittinger C.T., Carroll S.B.;
RT "Evolution of key cell signaling and adhesion protein families
RT predates animal origins.";
RL Science 301:361-363(2003).
DR EMBL; AF440359; AAL33602.2; -; mRNA.
DR HSP; P08581; IRIW.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000152; Aex\_hydroxyl\_S.
DR InterPro; IPR000742; EGF\_2.
DR InterPro; IPR001881; EGF\_Ca.
DR InterPro; IPR006209; EGF\_like.
DR InterPro; IPR003006; Ig\_MHC.
DR InterPro; IPR000719; Prot\_kinase.
DR InterPro; IPR000436; Sushi\_SCR\_CCP.
DR InterPro; IPR001245; Tyr\_pkinase.
DR InterPro; IPR008266; Tyr\_pkinase\_AS.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF07645; EGF\_CA; 1.
DR Pfam; PF00084; Sushi; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot\_kinase; 1.
DR SMART; SM00179; EGF\_CA; 1.
DR SMART; SM00219; TyRkC; 1.
DR PROSITE; PS0010; ASX\_HYDROXYL; 1.
DR PROSITE; PS00022; EGF\_1; 2.
DR PROSITE; PS01186; EGF\_2; 1.
DR PROSITE; PS00026; EGF\_3; 3.
DR PROSITE; PS01187; EGF\_CA; 1.
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.
DR PROSITE; PS00923; SUSHI; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1476 AA; 157129 MW; BEF0A03DDC3AD897 CRC64;

Query Match 28.1%; Score 56.5; DB 2; Length 1476;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 15; Indels 3; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQ-----RCSSNTPLPTCQ 31
: : : : : : : : : : : : : :
Db 110 CTISRNPSDLPPSCVCPPLNTARQDNHAEATCQ 143

RESULT 61
Q51EF3\_ENTHI PRELIMINARY; PRT; 1704 AA.
AC Q51EF3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protein kinase, putative.
GN ORFNames=10.t00023;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI\_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Anedeo P., Roncaglia P., Beriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Sun B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
RA Chillingworth T., Church C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Slicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RL "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AAFB01000050; BALS1244.1; -; Genomic\_DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR006212; Furin\_repeat.
DR InterPro; IPR000719; Prot\_kinase.
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.
DR InterPro; IPR002290; Ser\_thr\_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot\_kinase; 1.
DR SMART; SM00261; FU; 6.
DR SMART; SM00220; S\_TKc; 1.
DR SMART; SM00219; TyRkC; 1.
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1704 AA; 195112 MW; 0FDF183DA12770E3 CRC64;

Query Match 28.1%; Score 56.5; DB 2; Length 1704;
Best Local Similarity 39.4%; Pred. No. 2e+02;
Matches 13; Conservative 3; Mismatches 12; Indels 5; Gaps 1;

Qy 6 YFDSLHACIPQ-----LRCSNTPLPTCQRY 33
: : : : : : : : : : : : : :
Db 754 YFEHKFSCTCDGLFTNCCSSINVLVCQSY 786

RESULT 62
Q60WC9\_CAEBR PRELIMINARY; PRT; 135 AA.
AC Q60WC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG19174;
GN Name=CBG19174;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI\_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000098; CAE72086.1; -; Genomic\_DNA.
DR InterPro; IPR006209; EGF\_like.
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.
DR Pfam; PF01826; TIL; 2.
DR PROSITE; PS01196; EGF\_2; UNKNOWN\_2.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14981 MW; 74B21060EAF539B6 CRC64;

Query Match 27.9%; Score 56; DB 2; Length 135;
Best Local Similarity 37.1%; Pred. No. 17;
Matches 13; Conservative 3; Mismatches 13; Indels 6; Gaps 2;

Qy 1 CSQNEYFDSLHACIP-CQLRCSSNTPLPTCQRYC 34



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DR GO: 0007276; P:gametogenesis; IDA.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF00096; zf-C2H2; 3.
DR ProDom: PD000003; Znf_C2H2; 2.
DR SMART: SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFPC CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred. No. 45;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPLTCQRYC 34
Db 60 CNEREWESQLIRSLPHEGVRCPSQLAPIPFQNYC 93

RESULT 65
Q6P233_MOUSE
ID Q6P233_MOUSE PRELIMINARY; PRT; 341 AA.
AC Q6P233;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Zinc finger protein 393.
GN Name=Zfp393;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Aramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RG NIH WGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064748; AAH64748.1; -; mRNA.
DR Ensembl; ENSMUSG00000048626; Mus musculus.
DR MGI; MGI:2181068; Zfp393.
DR GO: 0007276; P:gametogenesis; IDA.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
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SQ SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred. No. 45;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPLTCQRYC 34
Db 60 CNEREWESQLIRSLPHEGVRCPSQLAPIPFQNYC 93

RESULT 66
Q9PVD4_XENLA
ID Q9PVD4_XENLA PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE P75-like transmembrane protein fullback (Neurotrophin receptor-related
protein la).
GN Name=NRH1a;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15258592; DOI=10.1038/ncb1158;
RA Sasai N., Nakazawa Y., Haraguchi T., Sasai Y.;
RT "The neurotrophin-receptor-related protein NRH1 is essential for
convergent extension movements.";
RL Nat. Cell Biol. 6:741-748(2004).
DR EMBL; AF131890; AADS4072.1; -; mRNA.
DR EMBL; AB162703; BAD36761.1; -; mRNA.
DR HSSP; P07174; INGR.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0005515; F:protein binding; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0006915; P:apoptosis; IEA.
DR GO: 0007165; P:signal transduction; IEA.
DR InterPro: IPR000488; Death.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 27.9%; Score 56; DB 2; Length 387;
Best Local Similarity 25.4%; Pred. No. 51;
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPLTCQRYC 31
Db 103 CPERQYLDLS-NGICLPQLCSKGHVVSQCTHNKNTVCQLCSSGFYSEVKSSSPCLPCR 161

QY 32 RYC 34
Db 162 TEC 164

RESULT 67
Q4KLX7_XENLA
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LOC398134 protein (Fragment).

DE Name=LOC398134; (African clawed frog).  
GN Xenopus laevis  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OOC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
NCBI\_TaxID=8355;  
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RZ MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Hopkins S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP  
RC TISSUE=Embryo;  
RZ MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
initiative.";  
Dev. Dyn. 225:384-391(2002).  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RP  
RC TISSUE=Embryo;  
RZ Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
RX EMBL; BC068640; AAH68640.1; -, mRNA.  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0005515; F:protein binding; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0006915; P:apoptosis; IEA.  
DR GO: GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
FT NON\_TER  
SQ SEQUENCE 392 AA; 42538 MW; 0B41CED6CC8080FB CRC64;  
Query Match 27.9%; Score 56; DB 2; Length 392;  
Best Local Similarity 25.4%; Pred. No. 52;  
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;  
QY 1 CSQNEYFDSLHACIPQL-----RC-----SSNTPPLTCQ 31  
DB 108 CPERQYLDLS-NGICLPQLCSKGHVVSQCTHNKNTVQLCSCGFYSEVKSSESPLPCR 166  
QY 32 RYC 34





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FT CARBOHYD 2122 2122 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 2165 2165 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 2178 2178 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 2329 2329 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 2359 2359 By similarity
FT DISULFID 2370 2381 By similarity
FT DISULFID 2375 2390 By similarity
FT DISULFID 2392 2401 By similarity
FT CONFLICT 823 823 C -> V (in Ref. 1; AA sequence)
FT CONFLICT 923 923 S -> Y (in Ref. 1; AA sequence)
FT CONFLICT 965 965 W -> Y (in Ref. 1; AA sequence)
FT CONFLICT 1241 1241 S -> K (in Ref. 1; AA sequence)
SQ SEQUENCE 2476 AA; 270365 MW; A13B690375A6548C CRC64;

Query Match
Best Local Similarity 31.6%; Pred. No. 3.4e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSONEYFDSLHACIP-CQ---LRCSNTPPLTCQRYC 34
Db 1851 CSAHSVTSCVPSCLPSCQDPGQCTGAGAPSTCEGC 1888

RESULT 71
Q9EP28_9HEPC PRELIMINARY; PRT; 146 AA.
AC Q9EP28;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN NUCLEOTIDE SEQUENCE.
RA Shinzawa H., Shao L., Jiang Q., Togashi H., Zhang X., Ishibashi M.,
RA Watanabe H., Saito T., Takahashi T., Ohba K., Mizokami M.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030968; BAB11770.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR CO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR002519; HCV env.
DR Pfam; PF01539; HCV env; I.
KW Envelope protein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 15763 MW; 9C67046FD8507C30 CRC64;

Query Match
Best Local Similarity 27.6%; Score 55.5; DB 2; Length 146;
Matches 14; Conservative 6; Mismatches 13; Indels 11; Gaps 3;

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Db 34 CSNNSITWLTDAVLHLPFCVPCESDNGTLRCWIQVTPNVAVKY 77

RESULT 72
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AC Q9VE40;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG714-PA (RH24988p).
GN ORFNAMES=CG714;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20156006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch L., Beasley E.M.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brattner P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RX Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426070; PubMed=12537573;
RX Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnik S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426069; PubMed=12537572;
RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
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Job time : 124.2 secs

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
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RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
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RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
DR .EMBL; AK056571; BAB71219.1; -; mRNA.  
DR .HSSP; P00743; ICCP.  
DR Ensembl; ENSG00000167992; Homo sapiens.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR001881; EGF Ca.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001304; Lectin C.  
DR InterPro; IPR001007; VWF C.  
DR Pfam; PF07645; EGF\_CA; 3.  
DR Pfam; PF00093; VWC; 5.  
DR SMART; SM00179; EGF\_CA; 3.  
DR SMART; SM00214; VWC; 6.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
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DR PROSITE; PS00026; EGF 3; 3.  
DR PROSITE; PS01187; EGF CA; 3.  
DR PROSITE; PS01208; VWF\_C; 1; UNKNOWN\_5.  
DR PROSITE; PS0184; VWF\_C\_2; 5.  
SQ SEQUENCE 955 AA; 9984 MW; 88B0DC8AABA9188 CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 955;  
Best Local Similarity 37.5%; Pred. No. 1.5e+02;  
Matches 12; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
QY 4 NEYFSLHACIPC-----QLRCSNTPPLTC 30  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 16:11:46 ; Search time 8.4 Seconds  
(without alignments)  
43.302 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51

Perfect score: 283

Sequence: 1 MLQACQCSQNEVFDLSLHA.....TPPLTCQRYCNASVTVSKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA.New:

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3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283	100.0	184	6	US-10-742-634-9
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3	230	81.3	40	6	US-10-967-527A-9
4	181	64.0	185	6	US-10-967-527A-10
5	71.5	25.3	249	6	US-10-967-527A-21
6	67.5	23.9	48	6	US-10-967-527A-20
7	67.5	23.9	292	6	US-10-967-527A-19
8	67.5	23.9	293	6	US-10-742-634-7
9	64.5	22.8	897	7	US-11-137-465-35
10	64.5	22.8	993	7	US-11-137-465-36
11	63	22.3	175	6	US-10-967-527A-7
12	55.5	19.6	1149	7	US-11-110-082-30
13	55.5	19.6	3690	6	US-10-995-561-1016
14	55.5	19.6	3714	6	US-10-995-561-1015
15	55.5	19.6	3717	6	US-10-821-234-1076
16	55.5	19.6	5405	7	US-11-108-172-1116
17	54.5	19.3	350	7	US-11-153-880-4
18	54.5	19.3	419	7	US-11-064-769-2
19	54.5	19.3	419	7	US-11-153-880-2
20	54.5	19.3	419	7	US-11-064-774A-22
21	54.5	19.3	997	7	US-11-113-424-37
22	54.5	19.3	1148	7	US-11-110-082-29
23	53	18.7	161	7	US-11-126-126-2
24	53	18.7	371	7	US-11-186-284-16
25	53	18.7	450	7	US-11-186-284-14
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					Sequence 8, Appl
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					Sequence 30, Appl
					Sequence 1016, Ap
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					Sequence 1076, Ap
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					Sequence 2, Appl
					Sequence 22, Appl
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					Sequence 29, Appl
					Sequence 2, Appl
					Sequence 16, Appl
					Sequence 14, Appl

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Sequence 14, Appl  
Sequence 556, App  
Sequence 1504, Ap  
Sequence 1412, Ap  
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Sequence 16, Appl  
Sequence 12, Appl  
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Sequence 186, App  
Sequence 272, App  
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Sequence 60, Appl

99	44.5	15.7	354	7	US-11-090-439-62	Sequence 62, Appl	172	41.5	14.7	1454	7	US-11-109-157A-2	Sequence 2, Appl1
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101	44.5	15.7	2339	7	US-11-096-281-11	Sequence 11, Appl	174	41.5	14.7	2491	6	US-10-995-561-769	Sequence 769, Appl
102	44	15.5	146	6	US-10-131-826A-408	Sequence 408, App	175	41	14.5	276	6	US-10-972-587-30	Sequence 30, Appl
103	44	15.5	215	6	US-11-116-144-297	Sequence 297, App	176	41	14.5	317	7	US-11-000-463-428	Sequence 428, App
104	44	15.5	236	6	US-10-467-657-8082	Sequence 8082, Ap	177	41	14.5	339	6	US-10-878-556A-18	Sequence 18, Appl
105	44	15.5	311	6	US-10-793-626-2450	Sequence 2450, Ap	178	41	14.5	339	6	US-10-995-561-681	Sequence 681, App
106	44	15.5	437	6	US-10-131-826A-466	Sequence 466, App	179	41	14.5	339	6	US-10-995-561-682	Sequence 682, App
107	44	15.5	456	6	US-10-641-678-55	Sequence 55, Appl	180	41	14.5	339	6	US-10-995-561-684	Sequence 684, App
108	44	15.5	497	6	US-10-454-437-410	Sequence 410, App	181	41	14.5	339	6	US-10-995-561-685	Sequence 685, App
109	44	15.5	500	7	US-11-067-573-2	Sequence 2, Appl1	182	41	14.5	339	6	US-10-995-561-686	Sequence 686, App
110	44	15.5	504	6	US-10-763-712A-78	Sequence 78, Appl	183	41	14.5	339	6	US-10-995-561-687	Sequence 687, App
111	44	15.5	514	7	US-11-186-284-228	Sequence 228, App	184	41	14.5	339	7	US-11-186-284-43	Sequence 43, Appl
112	44	15.5	636	7	US-11-029-003-8	Sequence 8, Appl1	185	41	14.5	344	6	US-10-821-234-923	Sequence 923, App
113	44	15.5	1028	6	US-11-067-121-7	Sequence 7, Appl1	186	41	14.5	495	6	US-10-873-528-99	Sequence 99, Appl
114	44	15.5	1036	6	US-10-131-826A-142	Sequence 142, App	187	41	14.5	712	6	US-10-995-561-984	Sequence 984, App
115	44	15.5	1255	6	US-10-770-726-62	Sequence 62, Appl	188	41	14.5	769	6	US-10-995-561-985	Sequence 985, App
116	44	15.5	1255	6	US-11-022-562-213	Sequence 213, App	189	41	14.5	769	6	US-10-995-561-986	Sequence 986, App
117	44	15.5	1255	7	US-11-113-202-10	Sequence 10, Appl	190	41	14.5	769	7	US-11-107-028-5	Sequence 5, Appl1
118	43.5	15.4	304	7	US-11-087-177-4	Sequence 4, Appl1	191	41	14.5	856	6	US-10-510-947-8	Sequence 8, Appl1
119	43.5	15.4	305	7	US-11-080-091-2	Sequence 2, Appl1	192	41	14.5	856	7	US-11-042-988-13	Sequence 13, Appl
120	43.5	15.4	305	7	US-11-087-177-7	Sequence 7, Appl1	193	41	14.5	859	7	US-11-000-463-423	Sequence 423, App
121	43.5	15.4	347	6	US-10-821-234-1081	Sequence 1081, Ap	194	41	14.5	859	7	US-11-000-463-895	Sequence 895, App
122	43.5	15.4	757	7	US-11-067-121-16	Sequence 16, Appl	195	41	14.5	934	7	US-11-108-864-19	Sequence 19, Appl
123	43.5	15.4	757	7	US-11-186-284-41	Sequence 41, Appl	196	41	14.5	1172	7	US-11-108-284-203	Sequence 203, App
124	43.5	15.4	1018	7	US-11-067-121-17	Sequence 17, Appl	197	41	14.5	1614	7	US-11-108-528-82	Sequence 82, Appl
125	43	15.2	42	6	US-10-467-657-7806	Sequence 6806, Ap	198	40.5	14.3	110	6	US-10-648-816-1	Sequence 1, Appl1
126	43	15.2	42	6	US-10-467-657-7828	Sequence 7828, Ap	199	40.5	14.3	110	6	US-10-648-816-2	Sequence 2, Appl1
127	43	15.2	186	6	US-10-467-657-470	Sequence 470, App	200	40.5	14.3	110	6	US-10-648-816-3	Sequence 3, Appl1
128	43	15.2	331	7	US-11-078-735-33	Sequence 33, Appl	201	40.5	14.3	110	6	US-10-648-816-4	Sequence 4, Appl1
129	43	15.2	332	7	US-11-078-735-51	Sequence 51, Appl	202	40.5	14.3	110	6	US-10-648-816-5	Sequence 5, Appl1
130	43	15.2	369	7	US-11-078-735-38	Sequence 38, Appl	203	40.5	14.3	110	6	US-10-648-816-6	Sequence 6, Appl1
131	43	15.2	397	6	US-10-878-556A-189	Sequence 189, App	204	40.5	14.3	110	6	US-10-648-816-7	Sequence 7, Appl1
132	43	15.2	337	6	US-10-995-561-928	Sequence 928, App	205	40.5	14.3	110	6	US-10-648-816-8	Sequence 8, Appl1
133	43	15.2	337	6	US-10-995-561-929	Sequence 929, App	206	40.5	14.3	239	6	US-10-980-388-108	Sequence 108, Appl
134	43	15.2	459	6	US-10-990-276-3	Sequence 3, Appl1	207	40.5	14.3	410	6	US-10-467-657-2312	Sequence 2312, Ap
135	43	15.2	484	7	US-11-078-735-43	Sequence 43, Appl	208	40.5	14.3	415	7	US-11-182-946-6	Sequence 6, Appl1
136	43	15.2	723	6	US-10-131-826A-346	Sequence 346, App	209	40.5	14.3	426	6	US-10-467-657-4808	Sequence 4808, Ap
137	43	15.2	723	7	US-11-078-735-17	Sequence 17, Appl	210	40.5	14.3	618	7	US-11-078-735-18	Sequence 18, Appl
138	43	15.2	1113	7	US-11-067-811-4	Sequence 4, Appl1	211	40.5	14.3	798	7	US-11-107-028-3	Sequence 3, Appl1
139	43	15.2	1210	7	US-11-113-202-6	Sequence 6, Appl1	212	40.5	14.3	1122	7	US-11-191-374-3	Sequence 3, Appl1
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141	43	15.2	1367	6	US-10-995-561-538	Sequence 538, App	214	40.5	14.3	3588	6	US-10-995-561-672	Sequence 672, App
142	43	15.2	1367	7	US-11-113-202-18	Sequence 18, Appl	215	40.5	14.3	4346	6	US-10-995-561-671	Sequence 671, App
143	43	15.2	1368	6	US-10-995-561-539	Sequence 539, App	216	40	14.1	47	7	US-11-000-463-408	Sequence 408, App
144	43	15.2	2725	7	US-11-113-424-52	Sequence 52, Appl	217	40	14.1	161	7	US-11-113-424-38	Sequence 38, Appl
145	42.5	15.0	160	6	US-10-846-172A-10	Sequence 10, Appl	218	40	14.1	196	6	US-10-995-561-579	Sequence 579, App
146	42.5	15.0	338	6	US-10-632-150-12	Sequence 12, Appl	219	40	14.1	219	6	US-10-995-561-580	Sequence 580, App
147	42.5	15.0	338	7	US-11-073-457-12	Sequence 12, Appl	220	40	14.1	250	6	US-10-131-826A-320	Sequence 320, App
148	42.5	15.0	338	7	US-11-073-460-12	Sequence 12, Appl	221	40	14.1	297	6	US-10-467-657-8438	Sequence 8438, Ap
149	42.5	15.0	526	6	US-10-606-302-5	Sequence 5, Appl1	222	40	14.1	334	6	US-10-995-561-822	Sequence 822, App
150	42.5	15.0	526	6	US-10-606-302-7	Sequence 7, Appl1	223	40	14.1	379	6	US-10-763-712A-40	Sequence 40, Appl
151	42.5	15.0	755	6	US-11-067-121-6	Sequence 6, Appl1	224	40	14.1	397	6	US-10-878-556A-165	Sequence 165, App
152	42.5	15.0	886	6	US-10-821-234-1390	Sequence 1390, Ap	225	40	14.1	414	6	US-10-131-826A-418	Sequence 418, App
153	42.5	15.0	1121	7	US-11-113-751-24	Sequence 24, Appl	226	40	14.1	418	6	US-10-312-954-4	Sequence 4, Appl1
154	42.5	15.0	1159	7	US-11-113-751-27	Sequence 27, Appl	227	40	14.1	421	6	US-10-763-712A-13	Sequence 13, Appl
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156	42	14.8	148	6	US-10-467-657-5478	Sequence 5478, Ap	229	40	14.1	447	6	US-10-632-150-10	Sequence 10, Appl
157	42	14.8	184	6	US-10-742-634-5	Sequence 5, Appl1	230	40	14.1	447	7	US-11-073-457-10	Sequence 10, Appl
158	42	14.8	184	6	US-10-967-527A-5	Sequence 5, Appl1	231	40	14.1	447	7	US-11-073-460-10	Sequence 10, Appl
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160	42	14.8	235	7	US-11-126-126-16	Sequence 16, Appl	233	40	14.1	727	6	US-10-995-561-864	Sequence 864, App
161	42	14.8	333	6	US-10-980-388-119	Sequence 119, App	234	40	14.1	782	6	US-10-995-561-861	Sequence 861, App
162	42	14.8	379	6	US-10-131-826A-308	Sequence 308, App	235	40	14.1	847	6	US-10-995-561-863	Sequence 863, App
163	42	14.8	444	7	US-11-029-003-16	Sequence 16, Appl	236	40	14.1	847	6	US-10-995-561-885	Sequence 885, App
164	42	14.8	461	7	US-11-132-285-6	Sequence 6, Appl1	237	39.5	14.0	72	6	US-10-467-657-4880	Sequence 4880, Ap
165	42	14.8	461	7	US-11-182-946-4	Sequence 4, Appl1	238	39.5	14.0	95	6	US-10-131-826A-62	Sequence 62, Appl
166	42	14.8	631	6	US-10-995-561-546	Sequence 546, App	239	39.5	14.0	118	7	US-11-116-144-158	Sequence 158, App
167	42	14.8	820	7	US-11-147-047-31	Sequence 31, Appl	240	39.5	14.0	143	6	US-10-821-234-1216	Sequence 1216, Ap
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169	41.5	14.7	395	7	US-11-075-185-13	Sequence 13, Appl	242	39.5	14.0	348	6	US-10-793-626-1702	Sequence 1702, Ap
170	41.5	14.7	830	6	US-10-995-561-899	Sequence 899, App	243	39.5	14.0	351	6	US-10-793-626-338	Sequence 338, App
171	41.5	14.7	842	6	US-10-645-441-2	Sequence 2, Appl1	244	39.5	14.0	386	6	US-10-131-826A-340	Sequence 340, App

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256 39.5 13.8 41 7 US-11-107-364-34  
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278 39.5 13.8 490 6 US-10-131-826A-310  
279 39.5 13.8 493 6 US-10-878-556A-65  
280 39.5 13.8 567 7 US-11-167-856-30  
281 39.5 13.8 585 7 US-11-108-172-1067  
282 39.5 13.8 620 6 US-10-131-826A-324  
283 39.5 13.8 637 7 US-11-154-324-4  
284 39.5 13.8 650 6 US-10-661-966-14  
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ALIGNMENTS

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; Publication No. US20050249671A9  
; GENERAL INFORMATION:  
; APPLICANT: Parmelee, David  
; APPLICANT: Yeh, Ren-Hwa  
; APPLICANT: Galperina, Olga  
; APPLICANT: Hilbert, David  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Th  
; FILE REFERENCE: 1488.1810002

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Sequence 1586, Ap  
Sequence 44, Appl

Query Match 100.0%; Score 283; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 9.8e-29;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 8, Application US/10967527A  
; Publication No. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor  
; TITLE OF INVENTION: Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967,527A  
; CURRENT FILING DATE: 2004-10-18  
; PRIOR APPLICATION NUMBER: 60/511,698  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-967-527A-8

Query Match 100.0%; Score 283; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 9.8e-29;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-967-527A-9  
; Sequence 9, Application US/10967527A  
; Publication No. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor  
; TITLE OF INVENTION: Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967,527A  
; CURRENT FILING DATE: 2004-10-18  
; PRIOR APPLICATION NUMBER: 60/511,698  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-967-527A-9

```
; LENGTH: 40
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(40)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-9

Query Match      81.3%; Score 230; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.4e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASV 45
DB      1 GQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASV 40

RESULT 4
US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

Query Match      64.0%; Score 181; DB 6; Length 185;
Best Local Similarity 70.8%; Pred. No. 4.7e-16;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4 MAQCQSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKG 51
DB      1 MAQCQCPHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46

RESULT 5
US-10-967-527A-21
; Sequence 21, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

Query Match      25.3%; Score 71.5; DB 6; Length 249;
Best Local Similarity 35.3%; Pred. No. 0.025; 13; Indels 1; Gaps 1;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYC 41
DB      6 CPKQDYWDSSRRKSCVSCALTCQRS-QRTCTDFC 38

RESULT 6
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-20

Query Match      23.9%; Score 67.5; DB 6; Length 48;
Best Local Similarity 30.6%; Pred. No. 0.019; 9; Indels 1; Gaps 1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNA 43
DB      13 CPEQYWDPELLGTSCMCKTICNHQS-QRTCAAFCRS 47

RESULT 7
US-10-967-527A-19
; Sequence 19, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 292
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-19

Query Match      23.9%; Score 67.5; DB 6; Length 292;
Best Local Similarity 30.6%; Pred. No. 0.092; 15; Indels 1; Gaps 1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNA 43
```



[illegible]

```

Query Match      22.3%; Score 63; DB 6; Length 175;
Best Local Similarity 50.0%; Pred. No. 0.21;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 QCSQNEYFDLSLHACIPCOL 26
Db 21 QCNQTECFDPLVRNCVSCEL 40

RESULT 12
US-11-110-082-30
; Sequence 30, Application US/11110082
; Publication No. US20050266558A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norriss, Michael Geoffrey
; APPLICANT: Saulsbury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074UC1
; CURRENT APPLICATION NUMBER: US/11/110,082
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/563,723
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 10/655,799
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1149
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-11-110-082-30

Query Match      19.6%; Score 55.5; DB 7; Length 1149;
Best Local Similarity 29.7%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 14 FDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVK 50
Db 632 FDSYVLAHV-CALSCELQFPFLCKNVTKSNIKDSIK 667

RESULT 13
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match      19.6%; Score 55.5; DB 6; Length 3690;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1844 ECAPGYRDVKGLFLGRVCPCQCHGHSRCLPGLSGVGVCDQHNTGHAHCEH-CQAGFVSS 1902

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RESULT 14
US-10-995-561-1015
; Sequence 1015, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match      19.6%; Score 55.5; DB 6; Length 3714;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1845 ECAPGYRDVKGLFLGRVCPCQCHGHSRCLPGLSGVGVCDQHNTGHAHCEH-CQAGFVSS 1903

RESULT 15
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1076
; LENGTH: 3717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076

Query Match      19.6%; Score 55.5; DB 6; Length 3717;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1866 ECAPGYRDVKGLFLGRVCPCQCHGHSRCLPGLSGVGVCDQHNTGHAHCEH-CQAGFVSS 1924

RESULT 16
US-11-108-172-1116
; Sequence 1116, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy

```

APPLICANT: Stolk, John A.  
APPLICANT: Wang, Tongtong  
APPLICANT: Jiang, Yugu  
APPLICANT: Smith, Carole L.  
APPLICANT: King, Gordon E.  
APPLICANT: Wang, Aijun  
APPLICANT: Clapper, Jonathan D.  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick Thomas S.  
APPLICANT: Carter, Darrick  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.471C15  
CURRENT APPLICATION NUMBER: US/11/108,172  
CURRENT FILING DATE: 2005-04-15  
PRIOR APPLICATION NUMBER: US 10/025,380  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: US 09/922,217  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 09/833,263  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: US 09/649,811  
PRIOR FILING DATE: 2000-08-28  
PRIOR APPLICATION NUMBER: US 09/609,448  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 09/575,251  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: US 09/519,444  
PRIOR FILING DATE: 2000-03-06  
PRIOR APPLICATION NUMBER: US 09/504,629  
PRIOR FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: US 09/480,321  
PRIOR FILING DATE: 2000-01-10  
PRIOR APPLICATION NUMBER: US 09/476,296  
PRIOR FILING DATE: 1999-12-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1130  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1116  
LENGTH: 5405  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-108-172-1116  
Query Match 19.6%; Score 55.5; DB 7; Length 5405;  
Best Local Similarity 33.3%; Pred. No. 41;  
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;  
Qy 7 QCSQNEYFDSLHACI-PCOLRCSSNTPPLTCQRYC 41  
Db 2732 ECPQNSHYE----LCADTCSLGCALSAPLQCPDGC 2763  
RESULT 17  
US-11-153-880-4  
Sequence 4, Application US/11153880  
Publication No. US20050256050A1  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/153,880  
FILING DATE: 16-Jun-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/219,442  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/999,811  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MARKOWICZ, KAREN R.  
REGISTRATION NUMBER: 36,351  
REFERENCE/DOCKET NUMBER: 1488.1000004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-11-153-880-4  
Query Match 19.3%; Score 54.5; DB 7; Length 350;  
Best Local Similarity 35.0%; Pred. No. 4.5;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;  
Qy 7 QCSQNEYFDSLHACI-PCOLRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACBCTES 296  
RESULT 18  
US-11-064-769-2  
Sequence 2, Application US/11064769  
Publication No. US20050256075A1  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Yl-Herttuala, Seppo  
APPLICANT: Hiltunen, Mikko O  
APPLICANT: Jeltsch, Markku M  
APPLICANT: Achen, Marc G  
TITLE OF INVENTION: Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis  
FILE REFERENCE: 28967/35601A  
CURRENT APPLICATION NUMBER: US/11/064,769  
CURRENT FILING DATE: 2005-02-24  
PRIOR APPLICATION NUMBER: US/09/427,657  
PRIOR FILING DATE: 1999-10-26  
PRIOR APPLICATION NUMBER: US 60/105,587  
PRIOR FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-064-769-2  
Query Match 19.3%; Score 54.5; DB 7; Length 419;  
Best Local Similarity 35.0%; Pred. No. 5.3;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;  
Qy 7 QCSQNEYFDSLHACI-PCOLRCSSNTP--PLTCQRYCNAS 44

Db 327 QCGANREFDNTCCV-CKRTCPNQLNPGKCACTES 365

RESULT 19

US-11-153-880-2

; Sequence 2, Application US/11153880

; Publication No. US20050256050A1

; GENERAL INFORMATION:

; APPLICANT: HU, JING-SHAN

; APPLICANT: ROSEN, CRAIG A.

; APPLICANT: CAO, LIANG

; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

; STREET: 1100 NEW YORK AVENUE

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.10

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/153,880

; FILING DATE: 16-Jun-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/219,442

; FILING DATE: 23-DEC-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/999,811

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/465,968

; FILING DATE: 08-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: MARKOWICZ, KAREN R.

; REGISTRATION NUMBER: 36,351

; REFERENCE/DOCKET NUMBER: 1488.1000004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)371-2600

; TELEFAX: (202)371-2540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 419 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-11-153-880-2

Query Match 19.3%; Score 54.5; DB 7; Length 419;

Best Local Similarity 35.0%; Pred. No. 5.3;

Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44

Db 327 QCGANREFDNTCCV-CKRTCPNQLNPGKCACTES 365

RESULT 20

US-11-064-774A-22

; Sequence 22, Application US/11064774A

; Publication No. US20050267024A1

; GENERAL INFORMATION:

; APPLICANT: Alitalo et al.

; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH FACTOR 2

; FILE REFERENCE: 28967/35977B2

; CURRENT APPLICATION NUMBER: US/11/064,774A

; CURRENT FILING DATE: 2005-02-24

; PRIOR APPLICATION NUMBER: 09/795,006

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: US 60/205,331

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: US 60/185,205

; PRIOR FILING DATE: 2000-02-25

; NUMBER OF SEQ ID NOS: 1212

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 22

; LENGTH: 419

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-064-774A-22

Query Match 19.3%; Score 54.5; DB 7; Length 419;

Best Local Similarity 35.0%; Pred. No. 5.3;

Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44

Db 327 QCGANREFDNTCCV-CKRTCPNQLNPGKCACTES 365

RESULT 21

US-11-113-424-37

; Sequence 37, Application US/11113424

; Publication No. US20050260713A1

; GENERAL INFORMATION:

; APPLICANT: Gangolli et al.

; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-225

; CURRENT APPLICATION NUMBER: US/11/113,424

; CURRENT FILING DATE: 2005-04-21

; PRIOR APPLICATION NUMBER: 60/256,704

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/311,590

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/257,314

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 60/311,613

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/315,617

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: 60/294,075

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 60/288,153

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 190

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 37

; LENGTH: 997

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-113-424-37

Query Match 19.3%; Score 54.5; DB 7; Length 997;

Best Local Similarity 28.2%; Pred. No. 12;

Matches 11; Conservative 4; Mismatches 11; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44

Db 751 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44

RESULT 22

US-11-110-082-29

; Sequence 29, Application US/11110082

; Publication No. US20050266558A1

```

; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norriess, Michael Geoffrey
; APPLICANT: Saulsbury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074Uc1
; CURRENT APPLICATION NUMBER: US/11/110,082
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/563,723
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 10/655,799
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Lolium perenne
; US-11-110-082-29

Query Match      19.3%; Score 54.5; DB 7; Length 1148;
Best Local Similarity 29.7%; Pred. No. 13;
Matches 11; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 14 FDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVK 50
Db 631 FDSVLAHV-CALSCQLPFLCKNVTKNIKDSIK 666

RESULT 23
US-11-126-126-2
; Sequence 2, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; TITLE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006-A
; CURRENT APPLICATION NUMBER: US/11/126,126
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 09/882,735
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 05/214,613
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,534
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-126-126-2

Query Match      18.7%; Score 53; DB 7; Length 161;
Best Local Similarity 33.3%; Pred. No. 3.4;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;

; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norriess, Michael Geoffrey
; APPLICANT: Saulsbury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074Uc1
; CURRENT APPLICATION NUMBER: US/11/110,082
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/563,723
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 10/655,799
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Lolium perenne
; US-11-110-082-29

Query Match      19.3%; Score 54.5; DB 7; Length 1148;
Best Local Similarity 29.7%; Pred. No. 13;
Matches 11; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 14 FDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVK 50
Db 631 FDSVLAHV-CALSCQLPFLCKNVTKNIKDSIK 666

RESULT 23
US-11-126-126-2
; Sequence 2, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; TITLE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006-A
; CURRENT APPLICATION NUMBER: US/11/126,126
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 09/882,735
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 05/214,613
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,534
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-126-126-2

Query Match      18.7%; Score 53; DB 7; Length 161;
Best Local Similarity 33.3%; Pred. No. 3.4;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;

; GENERAL INFORMATION:
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-186-284-16

Query Match      18.7%; Score 53; DB 7; Length 371;
Best Local Similarity 31.0%; Pred. No. 7.3;
Matches 13; Conservative 5; Mismatches 18; Indels 6; Gaps 2;

QY 3 QVAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNAS 44
Db 295 QFCGCLRNRYGEVRDALLDPNWHC-----PP--CRGICNCS 330

RESULT 25
US-11-186-284-14
; Sequence 14, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
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; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-14

Query Match      18.7%; Score 53; DB 7; Length 450;
Best Local Similarity 31.0%; Pred. No. 8.7;
Matches 13; Conservative 5; Mismatches 18; Indels 2; Gaps 2;

QY      3 QMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNAS 44
Db      374 QFCGPCLRNRYGVEVDALLDPNWHC-----PP--CRGICNCS 409

RESULT 26
US-11-182-946-3
; Sequence 3, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-3

Query Match      18.7%; Score 53; DB 7; Length 455;
Best Local Similarity 33.3%; Pred. No. 8.8;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;

QY      8 CSQNE---YFDSLHACIPCOLRCSSNTPPLTCQRYCNASVT 46
Db      127 CRKQYRHYWSENLFQCFNCSL-CLNGTVHLSCQEKQNTVCT 167

RESULT 27
US-11-076-187-4
; Sequence 4, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Fan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF355P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
```

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; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-4

Query Match      18.7%; Score 53; DB 7; Length 909;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;

QY      8 CSQNE---YFDSLHACIPCOLRCSSNTPPLTCQRYCNASVT 46
Db      125 CRKQYRHYWSENLFQCFNCSL-CLNGTVHLSCQEKQNTVCT 165

RESULT 28
US-11-137-465-43
; Sequence 43, Application US/11137465
; Publication No. US20050255558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-43

Query Match      18.4%; Score 52; DB 7; Length 1062;
Best Local Similarity 35.7%; Pred. No. 25;
Matches 10; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY      24 CQLRC----SSNTPPLTCQRYCNASVTN 47
Db      954 CNLRCLWLWGCSIPPFSCEDLCSALSCN 981
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 82
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-82

Query Match      17.5%; Score 49.5; DB 6; Length 406;
Best Local Similarity 34.3%; Pred. No. 22;
Matches 12; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

QY      6 GGCQNEYFDSLHACIPQLRCSNTPTLTQRY 40
DB      83 GGCIPEDY-DVCAEA--PCEQCTDNFGRVLCTCY 114

RESULT 33
US-10-995-561-1033
; Sequence 1033, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1033
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1033

Query Match      17.5%; Score 49.5; DB 6; Length 1798;
Best Local Similarity 26.8%; Pred. No. 84;
Matches 15; Conservative 4; Mismatches 12; Indels 25; Gaps 3;

QY      5 AGCQSQNEYFDSL-----HACIP-----CQL-RCSNTPTPL 35
DB      940 ATSCHQDEYSQQIVCHRCAGYTGRLRCEACAPGHGDPSPRGRCQLCECSGNIDPM 995

RESULT 34
US-10-995-561-1034
; Sequence 1034, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
;

; SEQ ID NO 1034
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1034

Query Match      17.5%; Score 49.5; DB 6; Length 1798;
Best Local Similarity 26.8%; Pred. No. 84;
Matches 15; Conservative 4; Mismatches 12; Indels 25; Gaps 3;

QY      5 AGCQSQNEYFDSL-----HACIP-----CQL-RCSNTPTPL 35
DB      940 ATSCHQDEYSQQIVCHRCAGYTGRLRCEACAPGHGDPSPRGRCQLCECSGNIDPM 995

RESULT 35
US-10-967-527A-18
; Sequence 18, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znf14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 42
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-18

Query Match      17.3%; Score 49; DB 6; Length 42;
Best Local Similarity 47.6%; Pred. No. 3.1;
Matches 10; Conservative 3; Mismatches 6; Indels 2; Gaps 2;

QY      8 CSQNEYFDSLHACIPCOLRC 28
DB      2 CQENEYWDQ-WGRCVTCQ-RC 20

RESULT 36
US-11-132-285-61
; Sequence 61, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
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; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-21

Query Match      17.3%; Score 49; DB 7; Length 1238;
Best Local Similarity 25.6%; Pred.No. 69;
Matches 11; Conservative 8; Mismatches 18; Indels 6; Gaps 1;

QY    5 AGQCQNEYFDSL-----LHACIPQLCRCSSNTPLTCORYC 41
      ||| : : ||| : : ||| : : ||| : : ||| : : |||
Db     169 AGMINPEDRWKSLHFSGHVHLEQLIRVRCDENYYSATCNKFC 211

RESULT 39
US-10-995-561-827
; Sequence 827, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 2107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-827

Query Match      17.3%; Score 49; DB 6; Length 2107;
Best Local Similarity 34.1%; Pred.No. 1.1e+02;
Matches 14; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

QY    7 QCQONEYF-----DSLLHACIPQLCRCSSNTPLTCORYC 41
      ||| : : ||| : : ||| : : ||| : : |||
Db     866 QCNLDLFSTPGSCDLSGSLICK-----PGTTGRYC 898

RESULT 40
US-11-080-991-94
; Sequence 94, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 2214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-94

Query Match      17.3%; Score 49; DB 7; Length 2214;

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```
Best Local Similarity 30.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 5; Mismatches 8; Indels 8; Gaps 1;

QY 21 CIPQRCSSNT-----PPLTCQRYCN 42
Db 1211 CIPQWACDGTDCQGSDEDPVCKCN 1240

RESULT 41
US-10-995-561-825
; Sequence 825, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 825
; LENGTH: 2480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-825

Query Match 17.3%; Score 49; DB 6; Length 2480;
Best Local Similarity 34.1%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

QY 7 QCSQNEYP-----DSLHACIPQCLRCSSNTPPLTCQRYC 41
Db 866 QCNDNLDFSPGSCDSLGSCLICK-----PGTTGRYC 898

RESULT 42
US-10-995-561-826
; Sequence 826, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 3116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-826

Query Match 17.3%; Score 49; DB 6; Length 3116;
Best Local Similarity 34.1%; Pred. No. 1.6e+02;
Matches 14; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

QY 7 QCSQNEYP-----DSLHACIPQCLRCSSNTPPLTCQRYC 41
Db 866 QCNDNLDFSPGSCDSLGSCLICK-----PGTTGRYC 898

RESULT 43
US-11-132-285-41
; Sequence 41, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
```

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FILE REFERENCE: PF511P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-41

Query Match 17.1%; Score 48.5; DB 7; Length 350;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY 6 GQCSONEY-----FDSL---LHACIPCO 25
Db 30 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCGSDTFTSRNNHLPACLSCN 89

QY 26 LRCSNTPPLTCQRYCNAS 44
Db 90 GRCDNQVE---TRSCNTT 105

RESULT 44
US-11-182-946-14
; Sequence 14, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-14

Query Match 17.1%; Score 48.5; DB 7; Length 355;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY 6 GQCSONEY-----FDSL---LHACIPCO 25
Db 28 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCGSDTFTSRNNHLPACLSCN 87

QY 26 LRCSNTPPLTCQRYCNAS 44
```



```
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 4655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-556

Query Match      17.0%; Score 48; DB 6; Length 4655;
Best Local Similarity 25.9%; Pred. No. 3.1e+02;
Matches 14; Conservative 8; Mismatches 18; Indels 14; Gaps 2;

QY 2 LQAG-----QCSQNEYFDSLHACIPQLRC-----SSNTPPLTCQRYC 41
Db 3500 LQLSGSTYCMPCSSQFLCANNKCIPIWVKCQDKCQDCSGDELALCPORFC 3553

RESULT 50
US-10-821-234-1504
; Sequence 1504, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1504
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1504

Query Match      16.8%; Score 47.5; DB 6; Length 419;
Best Local Similarity 37.0%; Pred. No. 39;
Matches 17; Conservative 3; Mismatches 17; Indels 9; Gaps 3;

QY 2 LQAGQCSQNEYFDSLH-----CIPCQLR--CSSNTPPLTCQRY 40
Db 181 LHMparVvANSgFDVLCHALESYTTLPHYLRSPCPFN--PIRrPAY 224

RESULT 51
US-10-821-234-1412
; Sequence 1412, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1412
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1412

Query Match      16.8%; Score 47.5; DB 6; Length 703;
Best Local Similarity 21.4%; Pred. No. 63;
Matches 12; Conservative 6; Mismatches 25; Indels 13; Gaps 2;

QY 7 QCSQNEYFDSLHACIP-----CQLRCSSNTPPLTCQRYCNASVTNSVKG 51
Db 383 ECKTGYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYLCS--CSVGPRLSVDG 436

RESULT 52
US-11-182-946-5
; Sequence 5, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-5

Query Match      16.6%; Score 47; DB 7; Length 427;
Best Local Similarity 30.0%; Pred. No. 46;
Matches 12; Conservative 5; Mismatches 19; Indels 4; Gaps 3;

QY 7 QCSQNEYFDSLHA--CIPCQLRCSSNTPPL--TCORYCNA 43
Db 148 ECPDGTYSDEANHVDPCLCTV--CEDTERQLRECTRWADA 186

RESULT 53
US-11-182-946-9
; Sequence 9, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-9

Query Match      16.6%; Score 47; DB 7; Length 595;
Best Local Similarity 29.1%; Pred. No. 62;
Matches 16; Conservative 6; Mismatches 19; Indels 14; Gaps 4;

QY 7 QCSQNEYFDSL--LHACIPC-----CQLRCSSNTPPLTCQ----RYCNASVTNS 48
```

```

US-11-022-562-340
; Sequence 340, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-340

Query Match      16.6%; Score 47; DB 7; Length 879;
Best Local Similarity 28.9%; Pred. No. 89;
Matches 11; Conservative 6; Mismatches 11; Indels

Qy      22 IPCOLRCSSNT-----PPLTCORYCNASVNSV 49
       :||:|:||
Db      430 VPCHIRQIINTHWKGVKNVLPPEGDLGTCNSTVTSLI 467

RESULT 56
US-11-067-811-1
; Sequence 1, Application US/11067811
; Publication No. US20050260688A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A
; APPLICANT: Enshell-Sciiffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-811-1

Query Match      16.6%; Score 47; DB 7; Length 1042;
Best Local Similarity 28.2%; Pred. No. 1e+02;
Matches 11; Conservative 9; Mismatches 17; Indels

Qy      8 CSONEYFDSLHLACIPCOLRCS--SNTPLPTCQRYCNAS 44
       |||:|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     269 CGRGNFILCASGICIPGLKCNGYNDCCDWSDEAHNCNS 307

RESULT 57
US-10-995-670-670
; Sequence 670, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CARDIOVASCULAR DISORDERS AND DRUG RESPON
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561

```

```
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 4347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-670
```

```
Query Match      16.6%; Score 47; DB 6; Length 4347;
Best Local Similarity 36.4%; Pred. No. 3.9e+02;
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 3 QWAGCQSQNEYFDSLHLHACIPC 24
Db 456 QWAGCPDGHFYLEHSAACLPC 477
```

## RESULT 58

```
US-10-821-234-1155
; Sequence 1155, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1155
; LENGTH: 4419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1155
```

```
Query Match      16.6%; Score 47; DB 6; Length 4419;
Best Local Similarity 36.4%; Pred. No. 3.9e+02;
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 3 QWAGCQSQNEYFDSLHLHACIPC 24
Db 528 QWAGCPDGHFYLEHSAACLPC 549
```

## RESULT 59

```
US-11-147-047-50
; Sequence 50, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
```

```
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-50
```

```
Query Match      16.4%; Score 46.5; DB 7; Length 487;
Best Local Similarity 23.7%; Pred. No. 60;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;
```

```
QY 8 CSQNEYFDSLHLHACIPCQ-----LRCSSNT 32
Db 242 CSPGHYNTTTHRCIRCPVGTYPQPEFGQNHCIICPGNT 279
```

## RESULT 60

```
US-10-770-726-66
; Sequence 66, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-66
```

```
Query Match      16.4%; Score 46.5; DB 6; Length 712;
Best Local Similarity 28.6%; Pred. No. 85;
Matches 12; Conservative 11; Mismatches 12; Indels 7; Gaps 3;
```

```
QY 1 MLWAGCQSQNEYFDSLHLHACIP-----CQLRCSNT-PPLT 36
Db 271 IVDFAGYCAQNGFY-CLVYGLPNGSLDLRLHLCQTQACPPLS 311
```

## RESULT 61

```
US-10-770-726-57
; Sequence 57, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-57

Query Match      16.4%; Score 46.5; DB 6; Length 883;
Best Local Similarity 30.3%; Pred. No. 1e+02;
```



```
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-11-147-047-51

Query Match      16.4%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY      8 CSONEYFDSLHACIPQC-----LRCSST 32
DB      743 CSPGHYNTTTHRCIRCPVGTGVPQFEGQNHCIICPGNT 780

RESULT 66
US-11-055-822-100
; Sequence 100, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158

; SEQ ID NO 100
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-100

Query Match      16.4%; Score 46.5; DB 7; Length 1045;
Best Local Similarity 30.4%; Pred. No. 1.2e+02;
Matches 14; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY      1 MLOWAGQC-SONEYFDSLHACIPQCRLCSSNTPLTCQRYCNASV 45
DB      711 MLTVQEVCSLSLVDAVDAALDAEIRAALNDPKDQPLANISV 756

RESULT 67
US-11-078-735-12
; Sequence 12, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-078-735-12

Query Match      16.3%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      19 HACIPQCRLCSSNTPLTCQRYC 41
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 68
US-11-078-735-13
; Sequence 13, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
```



RESULT 69  
 US-11-078-735-14  
 ; Sequence 14, Application US/11078735  
 ; Publication No. US20050261477A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMPION, BRIAN ROBERT  
 ; APPLICANT: LENNARD, ANDREW CHRISTOPHER  
 ; APPLICANT: MCKENZIE, GRAHAME JAMES  
 ; APPLICANT: TUGAL, TAMARA  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS  
 ; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS  
 ; FILE REFERENCE: 674525-2019  
 ; CURRENT APPLICATION NUMBER: US/11/078,735  
 ; CURRENT FILING DATE: 2005-03-10  
 ; PRIOR APPLICATION NUMBER: PCT/GB03/03908  
 ; PRIOR FILING DATE: 2003-09-09  
 ; PRIOR APPLICATION NUMBER: PCT/GB03/03285  
 ; PRIOR FILING DATE: 2003-08-01  
 ; PRIOR APPLICATION NUMBER: PCT/GB03/01525  
 ; PRIOR FILING DATE: 2003-04-04  
 ; PRIOR APPLICATION NUMBER: GB 0300234.2  
 ; PRIOR FILING DATE: 2003-01-07  
 ; PRIOR APPLICATION NUMBER: PCT/GB02/05137  
 ; PRIOR FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: PCT/GB02/05133  
 ; PRIOR FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: GB 0220912.0  
 ; PRIOR FILING DATE: 2002-09-10  
 ; PRIOR APPLICATION NUMBER: GB 0220913.8  
 ; PRIOR FILING DATE: 2002-09-10  
 ; NUMBER OF SEQ ID NOS: 51  
 ; SOFTWARE: PatentIn Ver. 3.3  
 ; SEQ ID NO 14  
 ; LENGTH: 63  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-11-078-735-14

```

RESULT 71
US-10-131-826A-296
; Sequence 296, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven

```



```
; SEQ ID NO 54
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Fusarium oxysporum
US-10-641-678-54

Query Match      16.3%; Score 46; DB 6; Length 514;
Best Local Similarity 41.0%; Pred. No. 73;
Matches 16; Conservative 3; Mismatches 16; Indels 4; Gaps 2;
```

```
QY      16 SLIHACIPQQLRCSSNT---PPLTCQRYCNCASVTNSVKG 51
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      9 SALIAAARAQQVCSLNTETKPAITWSK-CTSSGCSDVKG 46
```

```
RESULT 75
US-11-109-157A-18
; Sequence 18, Application US/11109157A
; Publication No. US20050277175A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: TRUNCATED ADAMTS MOLECULES
; FILE REFERENCE: 01997.030500.
; CURRENT APPLICATION NUMBER: US/11/109,157A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/562,685
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 938
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-157A-18
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Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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DB      630 CSAKTKPVTPEKICNA 645
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Search completed: December 21, 2005, 16:30:55  
Job time : 11.4 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 16:11:05 ; Search time 132.6 Seconds  
(without alignments)  
160.704 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51

Perfect score: 283

Sequence: 1 MLQMACQCSQNEFYDSLHA.....TPPLTCQRYCNASVINSVKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA.Main:

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- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB pep:\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	283	100.0	184	4	US-10-077-137-7
5	283	100.0	184	4	US-10-068-725-2
6	283	100.0	184	4	US-10-151-882-47
7	283	100.0	184	4	US-10-115-192-8
8	283	100.0	184	4	US-10-008-063-7
9	283	100.0	184	4	US-10-152-363A-27
10	283	100.0	184	4	US-10-216-074-11
11	283	100.0	184	4	US-10-087-080-39
12	283	100.0	184	4	US-10-742-634-9
13	283	100.0	184	5	US-10-626-914-6
14	283	100.0	184	5	US-10-485-489-6
15	283	100.0	184	5	US-10-861-049-27
16	283	100.0	184	5	US-10-989-826-46
17	283	100.0	184	6	US-11-021-874-27
18	283	100.0	302	4	US-10-115-192-12
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Sequence 13, Appl  
Sequence 11, Appl  
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149	61	21.6	246	6	US-11-021-874-53	Sequence 53, Appl	222	55.5	19.6	308	4	US-10-425-115-249202	Sequence 249202,
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; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215698
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

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; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
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; ORGANISM: Homo sapiens
US-10-008-063-7

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Best Local Similarity 100.0%; Pred. No. 2.3e-25;
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; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

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US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
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US-10-216-074-11

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; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1e1 Methods of Diagnosis of Metastatic Colorect
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-0008400S
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
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US-10-087-080-39
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FEATURE:  
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member  
; OTHER INFORMATION: 17 (TNFRSF17)  
US-10-087-080-39

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Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 12  
US-10-742-634-9  
; Sequence 9, Application US/10742634  
; Publication No. US20040208824A1  
; GENERAL INFORMATION:  
; APPLICANT: Parmelee, David  
; APPLICANT: Yeh, Ren-Hwa  
; APPLICANT: Galperina, Olga  
; APPLICANT: Hilbert, David  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Thereof  
; FILE REFERENCE: 1488.1810002  
; CURRENT APPLICATION NUMBER: US/10/742,634  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: US 60/435,262  
; PRIOR FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 60/467,198  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-742-634-9

Query Match 100.0%; Score 283; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 13  
US-10-626-914-6  
; Sequence 6, Application US/10626914  
; Publication No. US20050043516A1  
; GENERAL INFORMATION:  
; Patent Docket Preview  
; APPLICANT: CHUNTHARAPAI, ANAN  
; APPLICANT: GREWAL, IQBAL  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: YAN, MINHONG  
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof  
; FILE REFERENCE: P1942R1  
; CURRENT APPLICATION NUMBER: US/10/626,914  
; CURRENT FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US 60/398,530  
; PRIOR FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 6  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-626-914-6

Query Match 100.0%; Score 283; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 14  
US-10-485-489-6  
; Sequence 6, Application US/10485489  
; Publication No. US20050070689A1  
; GENERAL INFORMATION:  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Grewal, Iqbal  
; APPLICANT: Ridgway, John  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof  
; FILE REFERENCE: 11669.175USWO  
; CURRENT APPLICATION NUMBER: US/10/485,489  
; CURRENT FILING DATE: 2004-01-30  
; PRIOR APPLICATION NUMBER: PCT/US02/23487  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US 60/310,114  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/377,171  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 19  
; SEQ ID NO 6  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-489-6

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 15  
US-10-861-049-27  
; Sequence 27, Application US/10861049  
; Publication No. US20050095243A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040RIUS  
; CURRENT APPLICATION NUMBER: US/10/861,049  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 27  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-861-049-27

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVKG 51

Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51

RESULT 16  
US-10-989-826-46  
; Sequence 46, Application US/10989826  
; Publication No. US20050218650A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Crowley, Craig  
; APPLICANT: De Sauvage, Frederic J.  
; APPLICANT: Eaton, Daniel L.  
; APPLICANT: Ebens, Allen  
; APPLICANT: Polson, Andrew  
; APPLICANT: Smith, Victoria  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of  
; TITLE OF INVENTION: Hematopoietic Origin  
; FILE REFERENCE: P5105R1US  
; CURRENT APPLICATION NUMBER: US/10/989,826  
; CURRENT FILING DATE: 2004-11-16  
; PRIOR APPLICATION NUMBER: US 60/520,842  
; PRIOR FILING DATE: 2003-11-17  
; PRIOR APPLICATION NUMBER: US 60/532,426  
; PRIOR FILING DATE: 2003-12-24  
; NUMBER OF SEQ ID NOS: 75  
; SEQ ID NO 46  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-989-826-46

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51  
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51

RESULT 17  
US-11-021-874-27  
; Sequence 27, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1P1  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 27  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-27

Query Match 100.0%; Score 283; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51

Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51

RESULT 18  
US-10-115-192-12  
; Sequence 12, Application US/10115192  
; Publication No. US20030082175A1  
; GENERAL INFORMATION:  
; APPLICANT: Apotech R & D S.A.  
; APPLICANT: Biogen, Inc.  
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof  
; FILE REFERENCE: A083PCT  
; CURRENT APPLICATION NUMBER: US/10/115,192  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 60/215688  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/181807  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/157933  
; PRIOR FILING DATE: 1999-10-06  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-115-192-12

Query Match 100.0%; Score 283; DB 4; Length 302;  
Best Local Similarity 100.0%; Pred. No. 3.7e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51  
Db 24 MLQWAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 74

RESULT 19  
US-09-854-864-6  
; Sequence 6, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/Agp-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-6

Query Match 95.1%; Score 269; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.9e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 51  
Db 1 MAGCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTSVKG 48

RESULT 20  
US-09-855-158-6

; Sequence 6, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL  
; TITLE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-6

Query Match 95.1%; Score 269; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2,9e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48  
|||||

## RESULT 21

US-09-854-864-5  
; Sequence 5, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-5

Query Match 95.1%; Score 269; DB 3; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48  
|||||

## RESULT 22

US-09-855-158-5  
; Sequence 5, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL  
; TITLE OF INVENTION: 3, AND TACI

; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-5

Query Match 95.1%; Score 269; DB 3; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48  
|||||

## RESULT 23

US-09-854-864-9  
; Sequence 9, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-9

Query Match 95.1%; Score 269; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.6e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51  
|||||  
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 48  
|||||

## RESULT 24

US-09-855-158-9  
; Sequence 9, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12

```
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match      95.1%; Score 269; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTQRYCNASVTNSVKG 51
      |||||||
Db      1  MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTQRYCNASVTNSVKG 48

RESULT 25
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match      92.9%; Score 263; DB 4; Length 207;
Best Local Similarity 71.8%; Pred. No. 5.8e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Qy      1  MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPLTQRY 40
      |||||||
Db      39  MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCLHACIPQCLRCSSNTPLTQRY 98

RESULT 26
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Thompson, Jeffrey
```

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; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match      92.9%; Score 263; DB 4; Length 207;
Best Local Similarity 71.8%; Pred. No. 5.8e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Qy      1  MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPLTQRY 40
      |||||||
Db      39  MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCLHACIPQCLRCSSNTPLTQRY 98

RESULT 27
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8  CSQNEYFDSLHACIPQCLRCSSNTPLTQRYCNASVTNSVKG 51
      |||||||
Db      1  CSQNEYFDSLHACIPQCLRCSSNTPLTQRYCNASVTNSVKG 44

RESULT 28
US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
```

```
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match      88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 44

RESULT 29
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 30
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match      71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 31
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      71.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 32
US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-13
```

```
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match      88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 44

RESULT 29
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 30
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match      71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 31
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      71.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
      |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 32
US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-13
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;
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match      71.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 41
Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

RESULT 33
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match      64.0%; Score 181; DB 3; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.4e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKG 51
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46

RESULT 34
US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-855-158-11

Query Match      64.0%; Score 181; DB 3; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.4e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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```
Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKG 51
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46

RESULT 35
US-10-216-074-17
; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-074-17

Query Match      64.0%; Score 181; DB 4; Length 185;
Best Local Similarity 70.8%; Pred. No. 2.4e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKG 51
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46

RESULT 36
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match      64.0%; Score 181; DB 3; Length 281;
Best Local Similarity 70.8%; Pred. No. 3.6e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKG 51
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46
```

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RESULT 37
US-09-855-158-10
; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match 64.0%; Score 181; DB 3; Length 281;
Best Local Similarity 70.8%; Pred. No. 3.6e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGQCQSEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 1 MAQCCHSEYFDSLHACFCHLRCSN--PPATCQPCYCDPSVTSSVKG 46

RESULT 38
US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZHONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match 55.8%; Score 158; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGCQSEYFDSLHACIPQCLRC 28
Db 15 MLQWAGCQSEYFDSLHACIPQCLRC 42

RESULT 39
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
```

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FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 36.7%; Score 104; DB 3; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.00018;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

QY 9 SQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-QC--SVT-SVKG 34

RESULT 40
US-09-855-158-12
; Sequence 12, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLI
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-855-158-12

Query Match 36.7%; Score 104; DB 3; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.00018;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

QY 9 SQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-QC--SVT-SVKG 34

RESULT 41
US-10-087-192-1647
; Sequence 1647, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
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; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262,959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272,408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285,189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308,039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311,266  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/279,344  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 75  
; LENGTH: 5374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-107-782-75

Query Match 24.6%; Score 69.5; DB 4; Length 5374;  
Best Local Similarity 36.8%; Pred. No. 93;  
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;  
  
QY 7 QCSQNEYFDSLHACIP-COLRCSNTP--PLTCQRYC 41  
Db 3297 QCPTNSQFTDCLPSCVPCSNRCEVTSVPSSCREGC 3334

RESULT 45  
US-10-028-248A-74  
; Sequence 74, Application US/10028248A  
; Publication No. US20030235882A1  
; GENERAL INFORMATION:  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Vernet, Corine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Miller, Charles  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Zernhusen, Bryan  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Colman, Steven  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Si, Jingsheng  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Stone, David  
; APPLICANT: Sciore, Paul  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Rothenberg, Mark  
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods  
; FILE OF INVENTION: Thereof  
; FILE REFERENCE: 21402-222  
; CURRENT APPLICATION NUMBER: US/10/028,248A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/252959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285189

; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311266  
; PRIOR FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 74  
; LENGTH: 5376  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-028-248A-74

Query Match 24.6%; Score 69.5; DB 4; Length 5376;  
Best Local Similarity 36.8%; Pred. No. 93;  
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;  
  
QY 7 QCSQNEYFDSLHACIP-COLRCSNTP--PLTCQRYC 41  
Db 3299 QCPTNSQFTDCLPSCVPCSNRCEVTSVPSSCREGC 3336

RESULT 46  
US-10-107-782-74  
; Sequence 74, Application US/10107782  
; Publication No. US20040018970A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Casman, Stacie  
; APPLICANT: Colman, Steve  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Li, Li  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Miller, Charles  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Sciore, Paul  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Si, Jingsheng  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Stone, David  
; APPLICANT: Taupier, Raymond, Jr.,  
; APPLICANT: Tchernev, Velizar,  
; APPLICANT: Vernet, Corine,  
; APPLICANT: Zernhusen, Brian  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 21402-222CIP  
; CURRENT APPLICATION NUMBER: US/10/107,782  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 10/028,248  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262,959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272,408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285,189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308,039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311,266  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/279,344  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 74  
; LENGTH: 5376  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-107-782-74

Query Match 24.6%; Score 69.5; DB 4; Length 5376;  
Best Local Similarity 36.8%; Pred. No. 93; Mismatches 16; Indels 3; Gaps 2;  
Matches 14; Conservative 5

QY 7 QCSQNEVFDLSLLHACIP-CQLRCSSNTP--PLTCQRYC 41  
DB 3299 QCTNSQFTDCLFSCVPCSNRCVETSPVSSCREGC 3336

RESULT 47  
US-10-152-363A-62  
; Sequence 62, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; APPLICANT: Gross, Jane A.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 62  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion protein.  
US-10-152-363A-62

Query Match 24.2%; Score 68.5; DB 4; Length 332;  
Best Local Similarity 27.9%; Pred. No. 7.8;  
Matches 12; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

QY 1 MLQWAGCQSQNEVFDLSLLHACIP-CQLRCSSNTPPLTCQRYCNA 43  
DB 17 VLSAMRSCPEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCS 58

RESULT 48  
US-09-779-050A-45  
; Sequence 45, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 45  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-050A-45

Query Match 23.9%; Score 67.5; DB 3; Length 37;  
Best Local Similarity 30.6%; Pred. No. 1.2;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEVFDLSLLHACIP-CQLRCSSNTPPLTCQRYCNA 43

DB 2 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCS 36

RESULT 49  
US-09-854-864-20  
; Sequence 20, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 20  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-20

Query Match 23.9%; Score 67.5; DB 3; Length 59;  
Best Local Similarity 30.6%; Pred. No. 1.8;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEVFDLSLLHACIP-CQLRCSSNTPPLTCQRYCNA 43  
DB 1 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCS 35

RESULT 50  
US-09-855-158-20  
; Sequence 20, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 20  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-20

Query Match 23.9%; Score 67.5; DB 3; Length 59;  
Best Local Similarity 30.6%; Pred. No. 1.8;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEVFDLSLLHACIP-CQLRCSSNTPPLTCQRYCNA 43  
DB 1 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCS 35

RESULT 51  
US-09-854-864-15  
; Sequence 15, Application US/09854864



[illegible]

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; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-36

Query Match      23.9%; Score 67.5; DB 6; Length 265;
Best Local Similarity 30.6%; Pred. No. 8.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEFDSLHACIPCOLRCSSNTPLTCORYCNA 43
      : : : : : : : : : : : : : : : : : : :
Db      34 CPEEQYWDPLLGTCMCKTICNHQS-QRTCAAFCRS 68

RESULT 60
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match      23.9%; Score 67.5; DB 3; Length 291;
Best Local Similarity 30.6%; Pred. No. 8.9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEFDSLHACIPCOLRCSSNTPLTCORYCNA 43
      : : : : : : : : : : : : : : : : : : :
Db      34 CPEEQYWDPLLGTCMCKTICNHQS-QRTCAAFCRS 68

RESULT 61
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEFDSLHACIPCOLRCSSNTPLTCORYCNA 43
      : : : : : : : : : : : : : : : : : : :
Db      34 CPEEQYWDPLLGTCMCKTICNHQS-QRTCAAFCRS 68

RESULT 62
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEFDSLHACIPCOLRCSSNTPLTCORYCNA 43
      : : : : : : : : : : : : : : : : : : :
Db      34 CPEEQYWDPLLGTCMCKTICNHQS-QRTCAAFCRS 68

RESULT 63
US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

Query Match      23.9%; Score 67.5; DB 3; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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	Matches	11;	Conservative	9;	Mismatches	15;	Indels	1;	Gaps	1;
QY	8	CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA	43							
	:	:  :	:	:	:	:	:	:	:	:
DB	34	CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS	68							
	:	:  :	:	:	:	:	:	:	:	:
<b>RESULT 64</b>										
US-09-961-376-2										
; Sequence 2, Application US/09961376										
; Patent No. US20020106736A1										
; GENERAL INFORMATION:										
; APPLICANT: Ruben et al.										
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17										
; FILE REFERENCE: PF524P1										
; CURRENT APPLICATION NUMBER: US/09/961.376										
; CURRENT FILING DATE: 2001-09-25										
; PRIOR APPLICATION NUMBER: 60/254,874										
; PRIOR FILING DATE: 2000-12-13										
; PRIOR APPLICATION NUMBER: 60/235,991										
; PRIOR FILING DATE: 2000-09-26										
; PRIOR APPLICATION NUMBER: 09/533,822										
; PRIOR FILING DATE: 2000-03-24										
; PRIOR APPLICATION NUMBER: 60/188,208										
; PRIOR FILING DATE: 2000-03-10										
; NUMBER OF SEQ ID NOS: 7										
; SOFTWARE: PatentIn Ver. 2.1										
; SEQ ID NO 2										
; LENGTH: 293										
; TYPE: PRT										
; ORGANISM: Homo sapiens										
US-09-961-376-2										
Query Match 23.9%; Score 67.5; DB 3; Length 293;										
Best Local Similarity 30.6%; Pred. No. 9;										
Matches	11;	Conservative	9;	Mismatches	15;	Indels	1;	Gaps	1;	
QY	8	CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA	43							
	:	:  :	:	:	:	:	:	:	:	:
DB	34	CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS	68							
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<b>RESULT 65</b>										
US-09-779-050A-42										
; Sequence 42, Application US/09779050A										
; Patent No. US20020160416A1										
; GENERAL INFORMATION:										
; APPLICANT: BOYLE, WILLIAM										
; APPLICANT: HSU, HAILING										
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY										
; FILE REFERENCE: A-570B										
; CURRENT APPLICATION NUMBER: US/09/779,050A										
; CURRENT FILING DATE: 2001-02-12										
; PRIOR APPLICATION NUMBER: 60/181,800										
; PRIOR FILING DATE: 2000-02-11										
; NUMBER OF SEQ ID NOS: 52										
; SOFTWARE: PatentIn version 3.0										
; SEQ ID NO 42										
; LENGTH: 293										
; TYPE: PRT										
; ORGANISM: Homo sapiens										
US-09-779-050A-42										
Query Match 23.9%; Score 67.5; DB 3; Length 293;										
Best Local Similarity 30.6%; Pred. No. 9;										
Matches	11;	Conservative	9;	Mismatches	15;	Indels	1;	Gaps	1;	
QY	8	CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA	43							
	:	:  :	:	:	:	:	:	:	:	:
DB	34	CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS	68							
	:	:  :	:	:	:	:	:	:	:	:
<b>RESULT 66</b>										

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Best Local Similarity 30.6%; Pred.No.9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQLRCSNSTPPLTCORYCNA 43
       | : | : | : | : | : | : | : | : | :
Db      34 CPPEQWDPILGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 71
US-10-151-882-46
; Sequence 46, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

Query Match          23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred.No.9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQLRCSNSTPPLTCORYCNA 43
       | : | : | : | : | : | : | : | : | :
Db      34 CPPEQWDPILGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 72
US-10-293-816-2
; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match          23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred.No.9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPQLRCSNSTPPLTCORYCNA 43
       | : | : | : | : | : | : | : | : | :
Db      34 CPPEQWDPILGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 73
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US-10-008-063-8
; Sequence 8, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-8

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db      34 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 74
US-10-152-363A-2
; Sequence 22, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TAC1-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db      34 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCRS 68

RESULT 75
US-10-268-951-22
; Sequence 22, Application US/10268951
; Publication No. US20030166864A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
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; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db      34 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCRS 68

Search completed: December 21, 2005, 16:30:36
Job time : 137.6 secs
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Result No.	Score	Query			ID	Description
		Match	Length	PB		
1	283	100.0	184	2	US-09-565-423-11	Sequence 11, Appl
2	283	100.0	192	2	US-09-949-016-11115	Sequence 11115, A
3	269	95.1	51	2	US-09-854-864-6	Sequence 6, Appl
4	269	95.1	181	2	US-09-854-864-5	Sequence 5, Appl
5	269	95.1	283	2	US-09-854-864-9	Sequence 9, Appl
6	249	88.0	58	2	US-09-854-864-21	Sequence 21, Appl
7	201	71.0	34	2	US-09-854-864-7	Sequence 7, Appl
8	201	71.0	81	2	US-09-854-864-13	Sequence 13, Appl
9	181	64.0	185	2	US-09-865-423-17	Sequence 17, Appl
10	181	64.0	185	2	US-09-854-864-11	Sequence 11, Appl
11	181	64.0	281	2	US-09-854-864-10	Sequence 10, Appl
12	104	36.7	117	2	US-09-854-864-12	Sequence 12, Appl
13	67.5	23.9	59	2	US-09-854-864-20	Sequence 20, Appl
14	67.5	23.9	166	1	US-08-810-572A-6	Sequence 6, Appl
15	67.5	23.9	166	2	US-09-290-333-6	Sequence 6, Appl
16	67.5	23.9	166	2	US-09-782-857A-6	Sequence 6, Appl
17	67.5	23.9	166	2	US-09-854-864-15	Sequence 15, Appl
18	67.5	23.9	293	1	US-08-810-572A-2	Sequence 2, Appl
19	67.5	23.9	293	2	US-09-290-333-2	Sequence 2, Appl
20	67.5	23.9	293	2	US-09-782-857A-2	Sequence 2, Appl
21	67.5	23.9	293	2	US-09-879-919-22	Sequence 22, Appl
22	67.5	23.9	293	2	US-09-848-295-4	Sequence 4, Appl
23	67.5	23.9	293	2	US-09-854-864-14	Sequence 14, Appl
24	67.5	23.9	397	2	US-09-854-864-18	Sequence 18, Appl
25	66.5	23.5	67	2	US-09-854-864-16	Sequence 16, Appl
26	64.5	22.8	581	2	US-10-104-047-2804	Sequence 2804, Appl
27	64.5	22.8	880	2	US-10-104-047-2834	Sequence 2834, Appl





```
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match      95.1%; Score 269; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51
DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 48

RESULT 4
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      95.1%; Score 269; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51
DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 48

RESULT 5
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match      95.1%; Score 269; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51
DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 48

RESULT 6
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      88.0%; Score 249; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51
DB 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 44

RESULT 7
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      71.0%; Score 201; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYC 41
DB 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYC 34

RESULT 8
US-09-854-864-13
```

```
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13
```

```
Query Match 71.0%; Score 201; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 9.2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
```

```
RESULT 9
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17
```

```
Query Match 64.0%; Score 181; DB 2; Length 185;
Best Local Similarity 70.8%; Pred. No. 5.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
```

```
QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46
```

```
RESULT 10
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
```

```
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11
```

```
Query Match 64.0%; Score 181; DB 2; Length 185;
Best Local Similarity 70.8%; Pred. No. 5.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
```

```
QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46
```

```
RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
```

```
Query Match 64.0%; Score 181; DB 2; Length 281;
Best Local Similarity 70.8%; Pred. No. 8.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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```
QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51
Db 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46
```

```
RESULT 12
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match          36.7%; Score 104; DB 2; Length 117;
Best Local Similarity 69.8%; Pred. No. 4.5e-05;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

QY 9 SONEYFDSLHACIPQLRCSSNTPLTCORYCNASVTHSVKG 51
Db 2 AQCEYWDPLLGTGCMSCCKTICNHQS-QRTCAAFCRS 34

RESULT 13
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCES: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match          23.9%; Score 67.5; DB 2; Length 59;
Best Local Similarity 30.6%; Pred. No. 0.47;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSONEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db 1 CPEEQYWDPLLGTGCMSCCKTICNHQS-QRTCAAFCRS 35

RESULT 14
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```



```

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-09-290-333-6
;
Query Match 23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLHACIFCQLRCSSNTPLTCQRYCNA 43
| : | | | | : | : | : | : | :
DB 34 CPBEQYWDPLLGTCSCKTICNHQS-QRTCAAFCS 68

RESULT 16
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; INVENTOR: Bulow, Gotz
; TITLE OF INVENTION: A LAMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-09-782-857A-6
;
Query Match 23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

```







```
RESULT 30
US-09-252-991A-18110
; Sequence 18110, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18110
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18110

Query Match 20.8%; Score 59; DB 2; Length 556;
Best Local Similarity 40.0%; Pred. No. 51;
Matches 14; Conservative 6; Mismatches 11; Indels 4; Gaps 2;

Qy 20 ACIPQLRCSSNTPLTCQ---RYCNASVTNSVKG 51
Db 503 ACPSSARRSASSPTACSWPRCCSAR-SSSVSG 536

RESULT 31
US-09-270-767-41037
; Sequence 41037, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41037
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41037

Query Match 20.7%; Score 58.5; DB 2; Length 670;
Best Local Similarity 42.9%; Pred. No. 72;
Matches 15; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

Qy 6 GOCQNEVFDLLHACIPQLRCSSNTPLTCQRY 40
Db 455 GRCFKNRQLSHLRYCKKCTI-CSSNI--LRCTRY 486

RESULT 32
US-09-270-767-56253
; Sequence 56253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56253
```

```
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56253

Query Match 20.7%; Score 58.5; DB 2; Length 670;
Best Local Similarity 42.9%; Pred. No. 72;
Matches 15; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

Qy 6 GOCQNEVFDLLHACIPQLRCSSNTPLTCQRY 40
Db 455 GRCFKNRQLSHLRYCKKCTI-CSSNI--LRCTRY 486

RESULT 33
US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-4

Query Match 20.5%; Score 58; DB 2; Length 1792;
Best Local Similarity 21.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

Qy 5 AGCQNEVFDLLHACIPQ-----LRCSNTPLTCQRYCNASVTNSV 49
Db 40 AEKCNAG-PPHTLSGECVPCDCNGSNECLDGSYCVHCQRNTTGEHCKELDGYIGDSI 98

Qy 50 KG 51
Db 99 RG 100

RESULT 34
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-8

Query Match 20.5%; Score 58; DB 2; Length 1800;
Best Local Similarity 21.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

Qy 5 AGCQNEVFDLLHACIPQ-----LRCSNTPLTCQRYCNASVTNSV 49
```



```
;
;
; Query Match 20.1%; Score 57; DB 2; Length 201;
; Best Local Similarity 31.1%; Pred. No. 30;
; Matches 14; Conservative 4; Mismatches 13; Indels 14; Gaps 3;

Qy 7 QCSQNEVFDLLHAC--IPQLRC-----SSNTPLTTCQRYCN 42
Db 33 KQENSSF-----ACPKNCSLESGYQMDNSGCPCECRNYCN 72

RESULT 40
US-09-589-892B-11
; Sequence 11, Application US/09589892B
; Patent No. 6689583
; GENERAL INFORMATION:
; APPLICANT: Jenuwein, Thomas
; APPLICANT: Laible, Gotz
; APPLICANT: O'Carroll, Donal
; APPLICANT: Eisenhaber, Frank
; APPLICANT: Rea, Stephen
; TITLE OF INVENTION: Chromatin-Regulator Genes
; FILE REFERENCE: 0652.1670001
; CURRENT APPLICATION NUMBER: US/09/589,892B
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 08/945,988
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: PCT/EP96/01818
; PRIOR FILING DATE: 1996-05-02
; PRIOR APPLICATION NUMBER: DE 195 16 776.7
; PRIOR FILING DATE: 1995-05-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-589-892B-11

Query Match 20.1%; Score 57; DB 2; Length 760;
Best Local Similarity 26.7%; Pred. No. 1.2e+02;
Matches 12; Conservative 8; Mismatches 23; Indels 2; Gaps 1;

Qy 2 LQAGQCSQNEVFDLL--HACICQLRCSSNTPLTTCQRYCNAS 44
Db 521 IQLKSSSNHVNYYTRCDHPGFCMDMNCSCIQTQNFCEKFCNCS 565

RESULT 41
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,967
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
```

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;
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-967-2

Query Match 19.8%; Score 56; DB 1; Length 2476;
Best Local Similarity 31.6%; Pred. No. 5.7e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 8 CSQNEVFDLLHACIP-CQ---LRCSNTPPLTTCQRYC 41
Db 1851 CSAHSVYVTSVPSCLPSCQDPCQCTGAGAPSTCEGC 1888

RESULT 42
US-10-037-417-6
; Sequence 6, Application US/10037417
; Patent No. 6903201
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
```

; PRIOR APPLICATION NUMBER: 60/305,060  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/318,405  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/318,700  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 3597  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-417-6

Query Match 19.8%; Score 56; DB 2; Length 3597;  
Best Local Similarity 27.1%; Pred. No. 8.5e+02;  
Matches 16; Conservative 5; Mismatches 20; Indels 18; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCOLR-----CSSNTPPLTCORYCNASVTNS 48  
Db 1825 ECAPGYRDVKGLFLGRCVPCQCHGHSRCLPQSGVGVCDQHNTEGAHCR-CQAGFVSS 1882

RESULT 43  
US-10-037-417-2  
; Sequence 2, Application US/10037417  
; Patent No. 6903201  
; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Alsbrook II, John P  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Grosse, William M  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Li, Li  
; APPLICANT: Gorman, Linda  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Sciore, Paul  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Stone, David J  
; APPLICANT: Boldog, Ferenc L  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Anderson, David W  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Miller, Charles E  
; APPLICANT: Eisen, Andrew J  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-235  
; CURRENT APPLICATION NUMBER: US/10/037,417  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/260,018  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 60/260,360  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/272,411  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/272,817  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/291,186  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 60/303,231  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/305,060  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/318,405

; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/318,700  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 3600  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-037-417-2

Query Match 19.8%; Score 56; DB 2; Length 3600;  
Best Local Similarity 27.1%; Pred. No. 8.5e+02;  
Matches 16; Conservative 5; Mismatches 20; Indels 18; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCOLR-----CSSNTPPLTCORYCNASVTNS 48  
Db 1828 ECAPGYRDVKGLFLGRCVPCQCHGHSRCLPQSGVGVCDQHNTEGAHCR-CQAGFVSS 1885

RESULT 44  
US-09-949-016-10932  
; Sequence 10932, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10932  
; LENGTH: 3647  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10932

Query Match 19.6%; Score 55.5; DB 2; Length 3647;  
Best Local Similarity 26.7%; Pred. No. 9.9e+02;  
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCORYCNASVTNS 48  
Db 1778 ECAPGYRDVKGLFLGRCVPCQCHGHSRCLPQSGVGVCDQHNTEGAHCR-CQAGFVSS 1836

RESULT 45  
US-08-718-388-9  
; Sequence 9, Application US/08718388  
; Patent No. 6271362  
; GENERAL INFORMATION:

; APPLICANT: MORIKAWA, MINORU  
; APPLICANT: HARADA, NAOKI  
; TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk



```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-388-9

Query Match 19.4%; Score 55.5; DB 2; Length 5405;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

QY 7 QCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
Db 2732 ECPQSHYE---LCADTCSLGCALSAPLQCPDGC 2763

RESULT 46
US-09-270-767-56958
; Sequence 56958, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56958
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56958

Query Match 19.4%; Score 55; DB 2; Length 142;
Best Local Similarity 29.2%; Pred. No. 36;
Matches 14; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCOR--YCNASVTNSV 49
Db 29 VATYCTGDIYDLSGLCYCVSRQVA---TPVAGCNRCQYATSTFFVNAV 72

RESULT 47
US-09-270-767-41714
; Sequence 41714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41714
; LENGTH: 392
; TYPE: PRT

; ORGANISM: Drosophila melanogaster
US-09-270-767-41714

Query Match 19.4%; Score 55; DB 2; Length 392;
Best Local Similarity 29.2%; Pred. No. 1.1e+02;
Matches 14; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCOR--YCNASVTNSV 49
Db 279 VATYCTGDIYDLSGLCYCVSRQVA---TPVAGCNRCQYATSTFFVNAV 322

RESULT 48
US-09-902-540-11984
; Sequence 11984, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11984
; LENGTH: 991
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11984

Query Match 19.4%; Score 55; DB 2; Length 991;
Best Local Similarity 26.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 9; Mismatches 24; Indels 8; Gaps 2;

QY 3 QMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTC-----QRYCNASVTNSVKG 51
Db 453 QVVSACAEDPE-DTALRGCVPRVRAIINTPTGCSIQAPLPDAVNAVGVPLTLTG 507

RESULT 49
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-12

Query Match 19.4%; Score 55; DB 2; Length 1792;
Best Local Similarity 22.6%; Pred. No. 5.3e+02;
Matches 14; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 5 AGQCSQNEYFDSLHACIPQ-----LRCSNTPPLTCORYCNASVTNSV 49
Db 40 AERCDAG-FFRTLSGECAPDCDCNGNSHECLDGSFCLHCQRNTTGEHCCKLDGYIGDSI 98
QY 50 KG 51
Db 99 RG 100
```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/999,811
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-999-811-4

Query Match 19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASVTNSV 49
DB 64 AERCDAG-FFRTLSGEAPDCDNGNSHECLDGSFGLHCQRNTTGEHCEKLDGYIGDSI 122

QY 50 KG 51
DB 123 RG 124

RESULT 51
US-09-270-767-32231
; Sequence 32231, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32231
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-32231

Query Match 19.3%; Score 54.5; DB 2; Length 145;
Best Local Similarity 27.8%; Pred. No. 42;
Matches 15; Conservative 3; Mismatches 23; Indels 13; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASVTNS 48
DB 12 QCHRRHTGTPHVTVCQGFARSYKLOQHMIHSGRYPKC-TYCEKSFTQS 64

RESULT 52
US-08-999-811-4
; Sequence 4, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/999,811
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-999-811-4

Query Match 19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNAS 44
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 296

RESULT 53
US-08-824-996-2
; Sequence 2, Application US/08824996B
; Patent No. 5935820
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
; TITLE OF INVENTION: Factor 2
; FILE REFERENCE: PFI12D1
; CURRENT APPLICATION NUMBER: US/08/824,996B
; CURRENT FILING DATE: 1997-03-27
; EARLIER APPLICATION NUMBER: 08/207,550
; EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-824-996-2

Query Match 19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
```

QY 7 QCSQNEYFDSLHACIPQLCRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 296

RESULT 54  
US-09-042-105-4  
; Sequence 4, Application US/09042105  
; Patent No. 6040157  
; GENERAL INFORMATION:  
; APPLICANT: HU, JING-SHAN  
; APPLICANT: ROSEN, CRAIG A.  
; APPLICANT: CAO, LIANG  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 NEW YORK AVENUE  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042.105  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,550  
; FILING DATE: 8-MAR-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/465,968  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: TO BE ASSIGNED  
; FILING DATE: 24-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERIC K. STEFFE  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-042-105-4

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLCRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 296

RESULT 55  
US-08-510-133A-33  
; Sequence 33, Application US/08510133A  
; Patent No. 6221839  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari

; Joukov, Vladomir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/510.133A  
; APPLICATION NUMBER: US/08/510.133A  
; FILING DATE: 01-Aug-1995  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28113/32863  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-08-510-133A-33

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLCRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 296

RESULT 56  
US-08-585-895-33  
; Sequence 33, Application US/08585895  
; Patent No. 6245530  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladomir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/585,895  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28113/33072  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-585-895-33

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44  
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

## RESULT 57

US-10-084-488-4  
Sequence 4, Application US/10084488  
Patent No. 6734285

## GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/084,488

APPLICATION NUMBER: US/10/084,488

FILING DATE: 28-Feb-2002

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/623,725

FILING DATE: 07-Sep-2000

APPLICATION NUMBER: US 09/042,105

FILING DATE: 13-MAR-1998

APPLICATION NUMBER: US 09/107,997

FILING DATE: 30-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: MICHELE M. WALES

REGISTRATION NUMBER: 43,975

REFERENCE/DOCKET NUMBER: PF112PCT3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301)309-8504

TELEFAX: (301)309-8439

INFORMATION FOR SEQ ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-084-488-4

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44  
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

## RESULT 58

US-08-999-811-2

Sequence 2, Application US/08999811

Patent No. 5932540

## GENERAL INFORMATION:

APPLICANT: HU, JING-SHAN

APPLICANT: ROSEN, CRAIG A.

APPLICANT: CAO, LIANG

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 NEW YORK AVENUE

CITY: WASHINGTON

STATE: DC USA

COUNTRY: USA

ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/999,811

FILING DATE: HEREWITH

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,550

FILING DATE: 8-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MARKOWICZ, KAREN R.

REGISTRATION NUMBER: 36,351

REFERENCE/DOCKET NUMBER: 1488.1000004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

LENGTH: 419 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-999-811-2

Query Match 19.3%; Score 54.5; DB 1; Length 419;

Best Local Similarity 35.0%; Pred. No. 1.3e+02;

Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44

DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

## RESULT 59

US-09-042-105-2

Sequence 2, Application US/09042105

Patent No. 6040157

## GENERAL INFORMATION:

APPLICANT: HU, JING-SHAN

APPLICANT: ROSEN, CRAIG A.

APPLICANT: CAO, LIANG

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,105  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,550  
FILING DATE: 8-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TO BE ASSIGNED  
FILING DATE: 24-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ERIC K. STEFFE  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-042-105-2

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 327 QCGANREFDENTCQCV-CKRTCPRNQLNPGKCAECTES 365

RESULT 60  
US-09-042-105-18  
Sequence 18, Application US/09042105  
Patent No. 6040157  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,105  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,550  
FILING DATE: 8-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TO BE ASSIGNED  
FILING DATE: 24-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ERIC K. STEFFE  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-042-105-18

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 327 QCGANREFDENTCQCV-CKRTCPRNQLNPGKCAECTES 365

RESULT 61  
US-08-795-430-8  
Sequence 8, Application US/08795430  
Patent No. 6130071  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:

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;
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA: 08/510,133
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-430-8

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDLSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
||| ||| :|: ||| ||| ||| ||| ||| ||| |||
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 62
US-08-510-133A-35
; Sequence 35, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,133A
; FILING DATE: 01-AUG-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/32863
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid

;
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA: 08/510,133
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-430-8

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDLSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44
||| ||| :|: ||| ||| ||| ||| ||| ||| |||
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 63
US-09-355-700-8
; Sequence 8, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; Helsinki University Licensing
; Alitalo, Kari (U.S. only)
; Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-NOV-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/34140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-355-700-8
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Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 64  
US-09-355-700-58  
; Sequence 58, Application US/09355700  
; Patent No. 6361946  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research  
; Helsink University Licensing  
; Alitalo, Kari (U.S. only)  
; Joukov, Vladimir (U.S. only)  
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/355,700  
; FILING DATE: 05-NOV-1994  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/795,430  
; FILING DATE: 05-FEB-1997  
; APPLICATION NUMBER: PCT/FI96/00427  
; FILING DATE: 01-AUG-1996  
; APPLICATION NUMBER: 08/671,573  
; FILING DATE: 28-JUN-1996  
; APPLICATION NUMBER: 08/601,132  
; FILING DATE: 14-FEB-1996  
; APPLICATION NUMBER: 08/585,895  
; FILING DATE: 12-JAN-1996  
; APPLICATION NUMBER: 08/510,133  
; FILING DATE: 01-AUG-1995  
; APPLICATION NUMBER: 08/340,011  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28967/34140  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 419 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: other  
; LOCATION: 156  
; OTHER INFORMATION: /note= "codon 156 can be anything other  
; than cysteine, or can be nothing"

; SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-09-355-700-58  
Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 65  
US-08-601-132-33  
; Sequence 33, Application US/08601132  
; Patent No. 6403088  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/601,132  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28113/33118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 419 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-601-132-33  
Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 66  
US-08-706-054A-3  
; Sequence 3, Application US/08706054A  
; Patent No. 6451764  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; TITLE OF INVENTION: VEGF-Related Protein  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,054A  
FILING DATE: 30-Aug-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/003491  
FILING DATE: 08-Sep-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: P-40,378  
REFERENCE/DOCKET NUMBER: P0963R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-706-054A-3

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 67  
US-09-313-299-3  
Sequence 3, Application US/09313299B  
Patent No. 6576608  
GENERAL INFORMATION:  
APPLICANT: Lee, James  
TITLE OF INVENTION: VEGF-RELATED PROTEIN  
FILE REFERENCE: P0963R1D1  
CURRENT APPLICATION NUMBER: US/09/313,299B  
CURRENT FILING DATE: 1999-05-17  
EARLIER APPLICATION NUMBER: US 08/706,054  
EARLIER FILING DATE: 1996-08-30  
EARLIER APPLICATION NUMBER: US 60/003,491  
EARLIER FILING DATE: 1995-09-08  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 3  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Human  
FEATURE:  
NAME/KEY: Human  
LOCATION: 1-419  
OTHER INFORMATION: Sequence source: VRP  
Patent No. 6576608  
US-09-313-299-3

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 68  
US-08-465-968-2  
Sequence 2, Application US/08465968E  
Patent No. 6608182  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Vascular Endothelial Growth Factor 2  
FILE REFERENCE: PF112P1  
CURRENT APPLICATION NUMBER: US/08/465,968E  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/207,550  
EARLIER FILING DATE: 1994-03-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-465-968-2

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 69  
US-08-671-573B-33  
Sequence 33, Application US/08671573B  
Patent No. 6645933  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Receptor Ligand  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/671,573B  
FILING DATE: 28-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33348  
TELECOMMUNICATION INFORMATION:



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; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-671-573B-33

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365

RESULT 70
US-09-438-046-14
; Sequence 14, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-14

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365

RESULT 71
US-09-631-092B-33
; Sequence 33, Application US/09631092B
; Patent No. 6730658
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: RECEPTOR LIGAND VEGF-C
; FILE REFERENCE: 28967/33348A
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; CURRENT APPLICATION NUMBER: US/09/631,092B
; CURRENT FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 08/671,573
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/601,132
; PRIOR FILING DATE: 1996-02-14
; PRIOR APPLICATION NUMBER: 08/585,895
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: 08/510,133
; PRIOR FILING DATE: 1995-08-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-092B-33

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365

RESULT 72
US-10-084-488-2
; Sequence 2, Application US/10084488
; Patent No. 6734285
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,488
; FILING DATE: 28-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/623,725
; FILING DATE: 07-Sep-2000
; APPLICATION NUMBER: US 09/042,105
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: US 09/107,997
; FILING DATE: 30-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF112PCT3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301)309-8504
; TELEFAX: (301)309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-084-488-2
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